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(54) Title: MODULATORS OF TISSUE REGENERATION

(57) Abstract

Proteins which are upregulated in injured or regenerating tissues, as well as the DNA encoding these proteins, are disclosed, as well as therapeutic compositions and methods of treatment encompassing these compounds.

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MODULATORS OF TISSUE REGENERATION

Related Applications

This is a continuation-in-part of prior U.S. Provisionals S.N. 60/047,490 and S.N. 60/047,491, both filed May 23, 1997. The teachings of both earlier-filed Provisional patent applications are incorporated herein by reference.

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Field of the Invention

The invention relates generally to gene expression products, including nucleic acids (e.g., RNAs) and polypeptides that are upregulated in injured or regenerating tissues. Further, the invention relates generally to cDNAs and other nucleic acids encoding polypeptides that are upregulated in injured or regenerating tissues.

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Background of the Invention

The processes of tissue development during embryogenesis, and of tissue repair and/or regeneration following injury or insult are presently the topic of intense investigation. Both processes involve a dynamic remodeling of tissue architecture, which is triggered and mediated by numerous biological interactions, including cell-cell contact, cell-matrix contact, release of soluble biological response modifiers, synthesis of structural components, and many other changes in cell phenotype, including changes in gene expression. Many of the factors involved in tissue genesis and in the response to tissue insult remain unknown or poorly understood.

Several systems have been developed for modeling the events triggered by insult to particular tissues, and/or by particular types of insult. For example, several investigators have described events occurring in mammalian kidney tissue exposed to an ischemia-reperfusion insult. The kidney is able to repair damage to the proximal tubule epithelium through a complex series of events involving cell death, proliferation of surviving proximal tubule epithelial cells, formation of poorly differentiated regenerative epithelium over the

denuded basement membrane, and differentiation of the regenerative epithelium to form fully functional proximal tubule epithelial cells (Wallin et al., Lab. Invest. 66:474-484, 1992; Witzgall et al., Mol. Cell. Biol. 13:1933-1942, 1994; Ichimura et al., Am. J. Physiol. 269:F653-662, 1995; Thadhani et al., N. Engl. J. Med. 334:1448-1460, 1996). Growth factors such as IGF, EGF, and HGF have been implicated in this process of repair, as has the endothelial cell adhesion molecule ICAM-1. However, the mechanisms by which the tubular epithelial cells are restored, either functionally and morphologically, remain poorly understood.

There accordingly is a need for an improved understanding of the biological processes of tissue repair or regeneration. That is, there is a need to identify factors that are indicative of the initiation, development and resolution of normal wound healing or normal biological response to tissue insult. Similarly, there is a need to identify factors that are indicative of pathologies of abnormal responses to tissue insult or other stimulus, including autoimmune or other dysregulation pathologies, as well as pathologies associated with abnormal tissue growth including neoplastic growth. Further, there is a need to identify factors that constitute appropriate targets for therapeutic intervention to stimulate, modulate, enhance, suppress or otherwise manipulate biological responses to tissue insult. Similarly, there is a need to identify factors that constitute appropriate targets for therapeutic intervention to manipulate abnormal or dysregulated responses to tissue insult or other stimulus, including abnormal tissue growth associated with cancer (neoplasia) and, conversely, abnormal tissue quiescence associated with degenerative diseases.

Summary of the Invention

It is an object of this invention to identify factors that are indicative of the initiation, development and resolution of normal wound healing or normal biological response to tissue insult. A specific object of this invention is to identify products (e.g., RNAs, cDNAs, polypeptides) of genes that are upregulated in the context of healing tissue, or in tissue exposed to insult or injury. A particular object is to identify products of genes that are upregulated in mammalian kidney tissue exposed to insult or injury, such as ischemia-

reperfusion injury. A second specific object of this invention is to identify products of genes that are upregulated in pathological conditions associated with abnormal responses to tissue insult or other stimulus, including autoimmune or other dysregulation pathologies, as well as pathologies associated with abnormal tissue growth including neoplastic growth.

5 A third specific object is to identify gene products that constitute appropriate targets for therapeutic intervention to stimulate, modulate, enhance, suppress or otherwise manipulate biological responses to tissue insult. A particular object is to identify gene products for therapeutic intervention to manipulate responses of mammalian kidney tissue to tissue injury, such as ischemia-reperfusion injury. A fourth specific object is to identify gene

10 products that constitute appropriate targets for therapeutic intervention to manipulate abnormal or dysregulated responses to tissue insult or other stimulus, including abnormal tissue growth associated with cancer (neoplasia) and, conversely, abnormal tissue quiescence associated with degenerative diseases. Thus, other particular objects of the invention include the identification of gene products as targets for therapeutic intervention

15 in the clinical management (including prophylaxis, maintenance and treatment) of kidney diseases, including diseases involving renal failure, and of cancers derived from or affecting renal tissue.

The present invention rests on the discovery that the expression levels of numerous genes, including many genes heretofore unknown and/or uncharacterized, are upregulated in mammalian kidney tissue that has been exposed to tissue insult or injury. More specifically, the present invention rests on the discovery of a novel class of Kidney Injury-associated Molecules (each member of the class is henceforth called a "KIM"). KIMs are polypeptides encoded by genes whose expression levels are upregulated in the mammalian kidney upon exposure to tissue injury, particularly after exposure to ischemia-reperfusion injury. Any KIM is useful as an indicator of tissue status (preferably renal tissue status) or of a change therein (e.g., exposure to tissue injury, or the occurrence or stage of a tissue repair process). Any KIM further is useful as a target for therapeutic intervention to manipulate, whether by an agonist or an antagonist, a normal or abnormal tissue response to insult or other stimulus.

The invention accordingly provides, in a first aspect, purified and isolated nucleic acid molecules encoding all or a unique fragment of a KIM. In one embodiment, the present nucleic acids are RNAs. In another, they are DNA molecules, such as cDNAs. In another embodiment, the invention provides the complementary strands of nucleic acids encoding all or a unique fragment of a KIM. In another embodiment, the invention provides nucleic acids (preferably DNAs) that hybridize under low or, preferably, high stringency conditions to any of the foregoing nucleic acids. In still another embodiment, the invention provides nucleic acids (preferably DNAs) which, but for the degeneracy of the genetic code, would hybridize to any of the foregoing nucleic acids. In some embodiments, a nucleic acid encoding all or a unique fragment of a KIM is an engineered (recombinant) nucleic acid, optionally in operative association with an expression control element or other regulatory element. In other embodiments, a nucleic acid encoding all or a unique fragment of a KIM is an antisense nucleic acid sufficient, when internalized within a cell, to disrupt expression of a cellular KIM gene.

Specific novel KIMs (and unique fragments thereof) of the present invention are coded for by nucleic acids having the sequences disclosed herein in TABLE 1 and in the Sequence Listing. Other specific KIMs (and unique fragments thereof) are coded for by nucleic acids having sequences that are degenerate variants of any of the KIM sequences set forth in TABLE 1 and in the Sequence Listing. Still other specific KIMs (and fragments) are coded for by nucleic acids that are substantially similar to (homologous to) any of the KIM sequences in TABLE 1 and in the Sequence Listing. Such KIMs are defined herein as variants of the disclosed novel KIM sequences. In some embodiments, the present nucleic acid encodes a chimeric polypeptide comprising a novel KIM-encoding sequence (i.e., a sequence encoding part or all of a KIM) fused to a non-KIM sequence. Thus, the invention provides nucleic acids encoding novel KIM fusion proteins, non-limiting examples of which include KIM polypeptides fused to a secretable leader polypeptide, an immunoglobulin polypeptide, a binding pair partner (e.g., avidin, GST), a toxin or toxoid (e.g., ricin, tetanus), an enzyme (preferably one for which a detectable substrate is available, e.g., alkaline phosphatase, horseradish peroxidase, luciferase), or

other detectable polypeptide (e.g., green fluorescent protein). Additional specific KIMs (and unique fragments thereof) are coded for by nucleic acids referred to in TABLE 2. It is believed that, in most to all instances, these specific molecules have not heretofore been appreciated to be KIMs.

5 In a second aspect, the invention provides a vector having a KIM-encoding nucleic acid inserted therein. In some embodiments, the vector is a biologically functional plasmid or viral DNA vector. In other embodiments, the vector is a retroviral vector.

In a third aspect, the invention provides a prokaryotic or eukaryotic host cell comprising an internalized vector having a KIM-encoding nucleic acid insert. The present 10 host cell provides intracellular means for producing (synthesizing, folding, processing, or secreting) a KIM polypeptide of the present invention.

In a fourth aspect, the invention provides a process for the production of a KIM polypeptide. The present production process includes growing a host cell of the invention under culture conditions sufficient for the production of polypeptides of vector origin, and 15 recovering an expressed KIM polypeptide.

In a fifth aspect, the invention provides a purified and isolated novel KIM polypeptide, preferably substantially free of non-KIM polypeptides or proteins. In some embodiments, the present polypeptide is a full-length polypeptide, i.e., a polypeptide corresponding to the full-length open reading frame of a novel KIM-encoding cDNA. In 20 other embodiments, the present polypeptide is a unique fragment of the full-length polypeptide. Thus, specific novel KIM polypeptides (and unique fragments thereof) of the present invention are coded for by nucleic acids having the sequences disclosed herein in TABLE 1 and in the Sequence Listing. Other specific novel KIM polypeptides of the present invention are variants of the disclosed novel KIM sequences, including without 25 limitation splice variants, truncation variants, and substitution variants. In some embodiments, the invention provides a chimeric polypeptide comprising a novel KIM polypeptide fused (preferably via a peptide bond) to a non-KIM polypeptide. Thus, the invention provides novel KIM fusion proteins, exemplified by the above-mentioned fusion

constructs. Of course, the invention also provides conjugated or derivatized novel KIM polypeptides, including without limitation detectable conjugates, imageable conjugates, radiolabeled conjugates, and toxin conjugates. In still other embodiments, the invention provides chimeric polypeptides, fusion proteins and conjugates comprising a polypeptide 5 appreciated herein as being a KIM (see TABLE 2).

In a sixth aspect, the invention provides an antibody that binds selectively to a KIM polypeptide. Preferably, the antibody is a monoclonal antibody (or an engineered derivative thereof) produced by conventional means from a hybridoma derived from splenocytes of an animal immunized with a KIM polypeptide of the present invention. In 10 some embodiments, the present antibody is conjugated or derivatized with a detectable moiety, toxin, imageable compound or radionuclide.

In a seventh aspect, the invention provides a pharmaceutical composition comprising a therapeutically effective amount of a KIM nucleic acid (e.g., an antisense nucleic acid); a KIM vector; a KIM polypeptide; a KIM fusion protein; a KIM-binding 15 antibody (also referred to as an anti-KIM antibody), dispersed, dissolved or otherwise suspended in a physiologically acceptable carrier, vehicle, solvent or excipient.

In an eighth aspect, the invention provides methods and kits for detecting, either qualitatively or quantitatively, KIM expression and/or KIM polypeptide. As disclosed herein, KIMs are upregulated by exposure of mammalian kidney (renal) tissue to insult or 20 injury, particularly ischemia-reperfusion injury. Thus, any KIM (or combination or panel thereof) can be used as an indicator of tissue status (preferably renal tissue status), or of a change therein, including without limitation exposure to tissue injury, the occurrence or stage of an injury process, the occurrence or stage of a tissue repair or regeneration process, or the occurrence of an abnormal tissue response to injury or other stimulus, such as an 25 autoimmune response or an abnormal proliferative response (e.g., a neoplastic response).

In one embodiment, the invention provides a detection method and kit for diagnosis, prognosis, staging, or monitoring of renal injury or of renal disease or of the effectiveness of therapy therefor. Some specific embodiments involve detecting and/or

measuring the concentration of one or more KIM polypeptides in serum, urine, or urine sediment of an individual (a mammal, preferably a human) afflicted with or at risk of developing renal injury or an impairment of renal function. Some such embodiments involve the use of at least one KIM polypeptide, anti-KIM antibody or conjugate thereof as elements of a reagent kit for immunoassay according to standard techniques. For present purposes, any KIM disclosed herein or identified as such herein can be used as a kit element, along with other elements for KIM detection. In other instances, such as where the detected KIM has biological or enzymatic activity, the kit can include reagents for detecting KIM activity, e.g., by enzyme assay. Other specific embodiments involve 5 detecting and/or measuring the level of expression of one or more KIM-encoding nucleic acids in renal cells in a kidney biopsy, or in cells shed into urine or urine sediment of an individual afflicted with or at risk of developing renal injury or an impairment of renal function. Some such embodiments involve the use of a nucleic acid (e.g., RNA or DNA) 10 encoding a KIM polypeptide, or a unique fragment thereof, or a probe nucleic acid capable of hybridizing to nucleic acid encoding a KIM, as elements of a reagent kit for hybridization assay according to standard techniques. As above, any KIM nucleic acid 15 disclosed herein or appreciated herein as such can be used as a hybridization kit element, along with other reagents for detection of hybridized nucleic acids.

In another embodiment, the invention provides a method and kit for diagnosis, 20 prognosis, staging or monitoring of an abnormal response of renal tissue to tissue injury or other stimulus, including an autoimmune response or an abnormal proliferative response, such as neoplasia arising from or affecting renal tissue. Some specific embodiments involve detecting and/or measuring the concentration of one or more KIM polypeptides in serum, urine, or urine sediment of an individual (a mammal, preferably a human) afflicted 25 with or at risk of developing renal injury or an impairment of renal function. Some such embodiments involve the use of at least one KIM polypeptide, anti-KIM antibody or conjugate thereof as elements of a reagent kit for immunoassay according to standard techniques. For present purposes, any KIM disclosed herein or identified as such herein can be used as a kit element, along with other elements for KIM detection. In other instances,

such as where the detected KIM has biological or enzymatic activity, the kit can include reagents for detecting KIM activity, e.g., by enzyme assay. Other specific embodiments involve detecting and/or measuring the level of expression of one or more KIM-encoding nucleic acids in cells present in a kidney biopsy, or in cells shed into urine or urine sediment of an individual afflicted with or at risk of developing renal injury or an impairment of renal function. Some such embodiments involve the use of a nucleic acid (e.g., RNA or DNA) encoding a KIM polypeptide, or a unique fragment thereof, or a probe nucleic acid capable of hybridizing to nucleic acid encoding a KIM, as elements of a reagent kit for hybridization assay according to standard techniques. As above, any KIM nucleic acid disclosed herein or appreciated herein as such can be used as a hybridization kit element, along with other reagents for detection of hybridized nucleic acids.

In a ninth aspect, the invention provides a method and reagent for imaging tissues, either *in vitro* or *in vivo*. In particular, the invention provides a method and reagent for imaging the presence, extent or severity of kidney injury or of kidney tissue repair or regeneration. Similarly, the invention provides a method and reagent for imaging the presence, extent, severity or stage of an abnormal response to tissue injury or other stimulus, such as autoimmunity or neoplasia, particularly neoplasia arising from or affecting renal tissue. The present invention also provides a method for targetting an imageable compound to cells or tissue expressing or producing a KIM. The present method involves the step of contacting cells or tissue with a detectable (e.g., imageable) KIM-binding reagent, which in some embodiments is an anti-KIM antibody or conjugate thereof, or a KIM fusion protein. In other embodiments, the detectable KIM-binding reagent is a nucleic acid of the invention (e.g., a probe or antisense nucleic acid) labeled with a radionuclide or other imageable compound. According to the present method, cells expressing or producing a KIM are visualized (imaged) by detecting the presence and/or location of an accumulation of the KIM-binding reagent. For imaging *in vivo*, the KIM-binding reagent is administered, by any appropriate route, to an individual (a mammal, preferably a human) suspected of harboring an imageable locus of KIM expression and/or production. Without being limited hereby, it is believed that the present method can be

used to detect the presence and/or location of a tissue mass (e.g., a tumor) abnormally producing or expressing a KIM.

In a tenth aspect, the invention provides methods for treating an individual (a mammal, preferably a human) afflicted with or at risk of developing a disease or condition contributed to or associated with a dysfunction or dysregulation of a KIM gene or protein. Further, the invention provides methods for treating an individual afflicted with or at risk of developing a disease or condition beneficially affected by therapeutic administration of a KIM protein. The present methods involve the step of administering to the individual a therapeutically effective amount of a KIM polypeptide, variant or fusion protein thereof, or, conversely, of an anti-KIM antibody. It is expected that such compounds will be useful in therapeutic methods which manipulate, e.g., stimulate or inhibit, biological responses that are dependent on KIM function.

In an eleventh aspect, the invention provides a method for inhibiting the growth of KIM-expressing tumor cells, involving the step of contacting the cells with an anti-KIM antibody, conjugated to a toxin or radionuclide. In an alternative embodiment, the method involves the step of contacting the cells with an antisense KIM nucleic acid that is sufficient to suppress or disrupt expression of a KIM gene in the tumor cells.

In a twelfth aspect, the invention provides a method of gene therapy. The present method involves the administration of a vector capable of directing the production of a KIM, to an individual afflicted with or at risk of a renal disorder, disease or injury. As a result of the present method, growth of new tissue, preferably renal tissue, is stimulated, or survival of existing tissue, preferably renal tissue, is promoted.

The foregoing and other objects, features, aspects and advantages of the present invention, as well as the invention itself, will be more fully understood from the following description of preferred embodiments.

Detailed Description of the Invention

The discovery, reported herein, of a novel class of Kidney Injury-related Molecules (KIMs) was made by analyzing differences in mRNA expression between normal adult mammalian kidneys, and kidneys in the process of regenerating following exposure to tissue insult (specifically, to ischemia-reperfusion injury). Two established techniques were used for this purpose: representational difference analysis (RDA), and suppression subtractive hybridization (SSH). Both techniques were used to assess cDNAs isolated from various timepoints, e.g., 48 hours, after the onset of ischemia. In these studies, the normal adult kidney material was isolated from sham-operated subjects. Both techniques resulted in the depletion of cDNAs which are common to both postischemic and to normal kidney samples, leaving a pool of cDNAs which are significantly expressed only in injured or regenerating kidney tissue. This pool likely contains cDNAs corresponding to genes that encode proteins involved in the injury process, *and* proteins involved in tissue repair or regeneration processes. Therefore, cDNAs isolated from the pool likely encode parts or all of proteins likely to be therapeutically beneficial for treatment or prophylaxis of tissue injury, especially renal injury. Several cDNA clones have been obtained, sequenced and characterized.

Selected Definitions

A "KIM protein", herein used synonymously with "KIM", is any protein or polypeptide encoded by mRNA which is selectively upregulated following injury to a kidney. One group of KIM proteins of interest includes those coded for by mRNA which is selectively upregulated at any time within one week following any insult which results in injury to renal tissue. Examples of times at which such upregulation might be identified include 10 hours, 24 hours, 48 hours or 96 hours following an insult. Examples of tissue insults include toxin exposure, hypoxia, hyperoxia, hemodynamic disruption, ischemia, reperfusion, or mechanical compression. Many different types of proteins fall within the KIM class, including cell surface proteins (e.g., ligands or counter-receptors involved in cell-cell or cell-matrix interactions), secreted proteins (e.g., diffusible biological response modifiers, such as growth factors, differentiation factors, survival factors and the like),

intracellular proteins (e.g., elements of a signalling pathway), and nuclear proteins (e.g., transcription factors).

A "KIM ligand" is any molecule which noncovalently and specifically binds to a KIM protein. Such a ligand can be a protein, peptide, steroid, antibody, amino acid derivative, or other type molecule, in any form, including naturally-occurring, recombinantly produced, or otherwise synthetic. A KIM ligand can be in any form, including soluble, membrane-bound, or part of a fusion construct with immunoglobulin, fatty acid, or other moieties. The KIM ligand may be an integrin. A membrane-bound KIM ligand can act as a receptor which, when bound to or associated with KIM, triggers a cellular response. In some interactions, a KIM may associate with a plurality of KIM ligands, or may associate with a KIM ligand as part of a complex with one or more other molecules or cofactors. In a situation where both the KIM and the KIM ligand are bound to cell membranes, the KIM may associate and react with KIM ligand which is bound to the same cell as the KIM, or it may associate and react with KIM ligand be bound to a second cell. Where the KIM ligation occurs between molecules bound to different cells, the two cells may be the same or different with respect to cellular type or origin, phenotypic or metabolic condition, or type or degree of cellular response (e.g., growth, differentiation or apoptosis) to a given stimulus. "KIM ligation" refers to the contact and binding of KIM with a KIM ligand.

A "unique fragment" of a nucleic acid means any fragment of sufficient length to have a sequence likely to be substantially unique in a mammalian genome. Thus, a unique fragment generally means an oligonucleotide at least 16 nucleotide bases in length. Similarly, a "unique fragment" of a polypeptide means any fragment of sufficient length to have an amino acid sequence likely to be substantially unique to a given mammalian protein, such as a KIM. Thus, a unique peptide fragment generally means a peptide at least 7 amino acids in length.

A "KIM variant" means a KIM whose sequence differs from a sequence disclosed herein by the presence of one or more internal or terminal insertions, deletions or substitutions of a nucleotide (when referring to KIM nucleic acids) or of an amino acid

(when referring to KIM polypeptides). Preferably, the KIM variant is "substantially similar" to the corresponding disclosed KIM, or to a unique fragment thereof. That is, the KIM variant is "homologous" to the corresponding disclosed KIM. "Substantially similar" or "homologous" variants are structurally similar to the corresponding disclosed KIM. Further, "substantially similar" or "homologous" variants have sufficient functional similarity to the corresponding disclosed KIM that they share one or more of the KIM's biological properties or functions (e.g., binding to a receptor or ligand, triggering of biological responses, transport of a metabolite, catalysis of a substrate, or the like). A KIM variant can be naturally occurring or synthesized or produced by routine techniques, such as molecular engineering techniques.

By "alignment of sequences" is meant the positioning of one sequence, either nucleotide or amino acid, with that of another, to allow a comparison of the sequence of relevant portions of one with that of the other. Generally, sequences are aligned using the GAP and BESTFIT programs, which are based on the teachings of Needleman et al. (J. Mol. Biol. 48:443-453, 1970), Smith et al. (Adv. Appl. Math. 2:482-489, 1981), and Rechard et al. (CABIOS 5:107-113, 1989). Generally, when a homologous variant of a KIM is aligned with the corresponding KIM polypeptide, it will share amino acids that contribute to the KIM's three dimensional structure, such as cysteine residues. Although the relative positions of cysteine residues is generally conserved in the variant sequence, homologous or functionally equivalent sequences can include functionally equivalent arrangements of the cysteines, including arrangements comprising amino acid insertions or deletions which alter the linear arrangement of the cysteines, but do not materially impair their relationship or ability to form disulfide bonds in the folded structure of the KIM protein. Therefore, minor internal gaps and amino acid insertions, such as occur in splice variants, are ignored when aligning sequences herein.

"Sequence homology", "percent (%) homology", "sequence similarity" and "percent (%) similarity" are used interchangeably herein, and refer to the *sum* of the percentage of residues (whether nucleotides or amino acids) that are, when aligned with a reference sequence, the same as the corresponding reference residues, *and* those that are,

when aligned, conservative substitutions for the corresponding reference residues. "Sequence identity" and "percent (%) identity" also are used interchangeably herein, and refer to the percentage of residues (whether nucleotides or amino acids) that are, when aligned with a reference sequence, the same as the corresponding reference residues. Both 5 sets of terms are used according to their definitions in Altschul et al. (1990), J. Mol. Biol. 215:403-410 and in the Basic Local Alignment Search Tool (BLAST) algorithm described therein. For present purposes, the algorithm gap weight is set at 3.0 and the length weight is set at 0.1.

"Hybridization" means the formation of a duplex nucleic acid molecule, in which 10 nucleotide bases of a first polynucleotide strand bind noncovalently with cognate nucleotide bases of a second polynucleotide strand. Generally, such noncovalent binding occurs in DNA only between adenine (A) and thymidine (T) bases, and guanosine (G) and cytosine (C) bases. In RNA, binding occurs only between A and uracil (U), and G and C. The apposition of non-cognate bases in a duplex nucleic acid molecule, e.g., A with C, 15 is termed a "mismatch" pairing. Under high stringency hybridization conditions, mismatches occur rarely in a given duplex nucleic acid molecule. Low stringency conditions permit the occurrence of some mismatches. Exemplary conditions which promote DNA hybridization, termed "hybridization conditions", include 6.0X sodium chloride/sodium citrate (SSC) at about 45°C, followed by a wash of 2.0X SSC at 50°C. 20 The salt concentration in the wash step can be selected from a low stringency wash of about 2.0X SSC at 50°C, to a high stringency wash of about 0.2X SSC at 50°C. In addition, the temperature in the wash step can be selected from a low stringency wash at room temperature, about 22°C, to a high stringency wash at about 65°C.

A "KIM agonist" is a molecule which can specifically trigger a cellular response 25 normally triggered by the interaction of KIM with a KIM ligand. A KIM agonist can be a KIM variant, or a specific antibody to KIM, or a soluble form of the KIM ligand.

A "KIM antagonist" is a molecule which can specifically associate with a KIM ligand or a KIM, thereby blocking or otherwise inhibiting KIM binding to the KIM ligand. The antagonist binds or inhibits cellular responses which would otherwise be

triggered by ligation of the KIM ligand with KIM or with a KIM agonist. Examples of KIM antagonists include certain KIM variants, KIM fusion proteins and specific antibodies to a KIM ligand or KIM.

“Isolated” refers to a condition in which a nucleic acid or polypeptide of the present invention is essentially free of other nucleic acids, polypeptides, or of other contaminants with which it might normally be found in nature, and as such exists in a form not found in nature.

“Substantially pure” refers to a condition in which a nucleic acid or polypeptide of the present invention is separated from other nucleic acids, polypeptides, or other 10 contaminants, particularly naturally occurring contaminants, that interfere with the ability to detect, visualize or isolate the nucleic acid or polypeptide of the invention, or that interfere with a biological function or property thereof. A substantially pure nucleic acid or polypeptide of the invention is not generally found in nature.

A “chemical derivative” of another molecule contains one or more additional 15 chemical or biochemical moieties not found naturally in association with the molecule. Such moieties may improve the molecule's solubility, absorption, biological half life, etc. The moieties may alternatively decrease the toxicity of the molecule, eliminate or attenuate any undesirable side effect of the molecule, etc. Moieties capable of mediating such effects are disclosed, for example, in Remington's Pharmaceutical Sciences, 16th ed., Mack Publishing Co., Easton, Penn. (1980).

Other terms used herein, including “antisense DNA”, “antisense probe”, “cloning”, “cDNA”, “cDNA library”, “DNA polymorphism”, “expression”, “gene”, “hybridoma”, “plasmid”, “probe”, “labeled”, “recombinant”, “host cells”, “transformed”, “transfected”, “vector”, and the like are used in the sense of their art-recognized meanings in the fields of 25 cell biology, cell culture, molecular biology, transgenic biology, microbiology, recombinant DNA or genetic engineering, and immunology. Such meanings are determined by consultation of one or more of the following widely available texts: Molecular Cloning, A Laboratory Manual, 2nd Ed. (Sambrook, Fritsch and Maniatis, eds.).

Cold Spring Harbor Laboratory Press, 1989; DNA Cloning, Volumes I and II (Glover, ed.), 1985; Oligonucleotide Synthesis (Gait, ed.), 1984; U.S. Patent 4,683,195, Mullis et al., invs.; Nucleic Acid Hybridization (Hames & Higgins, eds.), 1984; Transcription and Translation (Hames & Higgins, eds.), 1984; Culture of Animal Cells (Freshney), Alan R. Liss, publ., 1987; Immobilized Cells and Enzymes (IRL Press), 1986; A Practical Guide to Molecular Cloning (Perbal), 1984; Current Protocols in Molecular Biology, Wiley & Sons, publ., 1989; Methods in Enzymology, Academic Press, New York NY (especially Volumes 154 and 155); Gene Transfer Vectors for Mammalian Cells (Miller and Calos, eds.), Cold Spring Harbor Laboratory Press, 1987; Immunochemical Methods in Cell and Molecular Biology (Mayer and Walker, eds.), Academic Press, London, 1987; Handbook of Experimental Immunology, Volumes I-IV (Weir and Blackwell, eds.), 1986; and, Manipulating the Mouse Embryo, Cold Spring Harbor Laboratory Press, 1986.

Compounds of the Invention

Specific, novel KIMs discovered through RDA or SSH techniques are set forth below in TABLE 1 and in the Sequence Listing. TABLE 1 lists KIMs for which potential full length (PFL) cDNA clones were obtained. Also shown are the predicted polypeptide sequences encoded in the open reading frames (ORFs) of many of the newly discovered KIMs. In addition, TABLE 1 provides, where relevant, the subtracted amplified clone (SAC) designations and the PFL location(s) of partial sequences, many of which were reported in prior U.S. Provisional S.N. 60/047,490 and 60/047,491.

TABLE 1

SEQ. NO.	PFL	CLONE DESIGNATION	OPEN READING FRAME (OFR)	
			LOCATION	SEQ. ID #
# 3	HW011	HW011		
# 4	HW012	HW012	39..671	# 5
# 6	HW013	HW013		
# 7	HW014	HW014rev	175..804	# 8
# 9	HW015	HW15	11..2176	# 10
# 12	HW017	SAC_24091		
# 13	HW018 HW101	SAC_23880	86..1102	# 14
# 16	HW033	SAC_23901		
# 17	HW034	SAC_23897	91..837 3101..4162	# 18 # 19
# 20	HW035 HW112	SAC_24468		
# 21	HW036	SAC_24406		
# 22	HW037 HW102	SAC_24354	280..1422	
# 26	HW040	SAC_24520	481..2433	# 27
# 28	HW041	SAC_24317		
# 29	HW042 HW113	SAC_24017	8..889	# 30
# 31	HW043	SAC_24533	8..634	# 32
# 33	HW044	SAC_24216	24..1100	# 34
# 35	HW045	SAC_24028	9..1628	# 36
# 37	HW046	SAC_24036	9..1160	# 38
# 39	HW047	SAC_23915	8..511	# 40
# 42	HW050 HW109	SAC_24644	7..1326	# 43
# 44	HW051	SAC_24170	114..1505	# 45
# 46	HW052	SAC_24882	247..765	# 47
# 49	HW055	SAC_24449	214..1329	# 50
# 51	HW056	SAC_24326	8..523	# 52
# 53	HW057	SAC_23926	7..1023	# 54
# 55	HW059	SAC_24457	9..1271	# 56
# 57	HW061	SAC_24029	7..1422	# 58
# 61	HW069	SAC_24477	1360..1893	# 62
# 64	HW073	SAC_24456	9..1223	# 65
# 66	HW074	SAC_24464	7..300	# 67
# 68	HW075 HW117	SAC_24466		
# 69	HW076	SAC_24409		
# 71	HW080	SAC_24033		
# 72	HW082	SAC_24469	150..569	# 73
# 75	HW084	SAC_24854		
# 76	HW088	SAC_24336	9..686	# 77
# 78	HW089	SAC_24461	8..1006	# 79

TABLE 1, continued

SEQ. NO.	PFL	CLONE DESIGNATION	OPEN READING FRAME (ORF)	
			LOCATION	SEQ. ID #
# 80	HW090 HW118	SAC_24197	335 .. 937	# 81
# 82	HW092	SAC_24320		
# 83	HW093	SAC_24538	8 .. 1357	# 84
# 85	HW094	SAC_23896	255 .. 1238	# 86
# 87	HW095	SAC_23802	7 .. 876	# 88
# 89	HW096	NONE	295 .. 1302	# 90

Additional KIMs, which are believed to be related to (e.g., substantially similar to) known molecules also were obtained through RDA or SSH techniques, and are set forth in TABLE 2 and in the Sequence Listing. It is believed that few to none of these molecules were previously appreciated to be KIMs, i.e., to have relevance to tissue injury or repair processes, particularly in the kidney. TABLE 2 lists these KIMs along with their clone designations. Partial sequences of some of the cDNA clones listed below were also set forth in the priority document. Also shown are the name(s) and GENBANK accession numbers of the known genes to which these KIMs may be related.

TABLE 2

SEQ 1D #	DESIGNATION	RELATED GENE	Accession #
92	23798	Rat alpha 1A (1D) adrenergic receptor	M60654
93	23800	Rat N27	V30789
94	23801	Rat alpha-2mu globulin-related protein	X13295
95	23833	Rat contrapsin-like protease inhibitor related protein	X16359
96	23836	Rat Fit-1	V04319
97	23853	Rat tumor-associated antigen (pE4)	L12025
98	23906	Rat sulfated glycoprotein 2	X13231
99	23907	Mouse secreted protein (p85)	L33416
100	23916	Human Differentiation-dependent A4 protein	L09604

TABLE 2, continued

SEQ ID #	DESIGNATION	RELATED GENE	Accession #
101	23922	Rat manganese-containing superoxide dismutase	Y00497
102	24030	Rat heme oxygenase	J02722
103	24078	Rat tissue inhibitor of metalloproteinase 1 (TIMP1)	U16022
104	24105	Rat alpha 2- macroglobulin	J02635
105	24140	Rat Cathepsin D	X54467
106	24142	Rat lysozyme	L12458
107	24192	Mouse MAMA mRNA	X67809
108	24296	Rat transketolase	U09256
109	24445	Rat heat stable antigen CD24/Elongation factor 1	Z11531
110	24527	Cathepsin L	S85184
111	24540	Mouse endothelial monocyte-activating polypeptide 1	U41341
112	24623	Rat spleen thymosin beta4	K01334
1	HW010	Human semaphorin (CD100)	U60800
11	HW016	Mouse ribonucleotide reductase M2 subunit	M14223
15	HW032	Human S100C	D49355
24	HW038	Human splicing factor SF3a120	X85237
25	HW039	Annexin 11	M82802
41	HW049	Mouse u22 snoRNA host gene (UHG)	U40654
48	HW054	Rat myelin oligodendrocyte protein (MOG)	M99485
59	HW062	Mouse proliferation-associated protein 1	U43918
60	HW066	Human cleavage stimulation factor 50kd subunit	L02547
63	HW070	Human BRCA2 region mRNA sequence CG037	U50523

TABLE 2, continued

SEQ ID #	DESIGNATION	RELATED GENE	Accession #
70	HW078	Human G protein gamma-10 subunit	P50151
74	HW083	Rat ins-1 winged helix	P97691
91	HW097	Human Na ⁺ channel 2	U78181

Any of the foregoing KIM cDNAs can be inserted into a vector, liposome or other carrier vehicle for internalization and production in a host cell. Furthermore, the invention
 5 encompasses derivatives and variants of each of the foregoing KIMs as listed in TABLES 1 and 2.

One embodiment of the invention provides soluble variants of a KIM protein that is usually synthesized as a membrane associated protein. Soluble variants lack at least a portion of the transmembrane or intra-membrane section of a native KIM protein. In some
 10 examples, the soluble variant lacks the entire transmembrane or intra-membrane section of a native KIM protein. Soluble variants include fusion proteins which encompass derivatives of KIM proteins that lack at least a portion of the transmembrane or intra-membrane section of a native KIM protein. All types of KIM fusion proteins are included, particularly those which incorporate his-tag, Ig-tag, and myc-tag forms of the molecule.
 15 These KIM fusions may have characteristics which are therapeutically advantageous, such as the increased half-life conferred by the Ig-tag. Also included are fusion proteins which incorporate portions of selected domains of the KIM protein.

Variants can differ from a naturally occurring KIM protein in amino acid sequence or in ways that do not involve sequence, or both. Variants in amino acid sequence are
 20 produced when one or more amino acids in naturally occurring KIM protein is substituted with a different natural amino acid, an amino acid derivative or non-natural amino acid. Particularly preferred substitution variants include naturally occurring KIM proteins, or biologically active unique fragments thereof, whose sequences differ from the wild type sequence by one or more conservative amino acid substitutions, which typically have
 25 minimal influence on the secondary structure and hydrophobic nature of the protein or

peptide. Conservative substitutions typically include the substitution of one amino acid for another with similar characteristics, such as substitutions within the following groups: valine, glycine; glycine, alanine; valine, isoleucine; aspartic acid, glutamic acid; asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine.

- 15 Other conservative substitutions are those which meet the criteria for an "accepted point mutation" as defined in the Atlas of Protein Sequence and Structure (Dayhoff et al., eds.), 1978. See also PCT publication no. WO97/44460.

Substitution variants can also have sequences which differ by one or more non-conservative amino acid substitutions, provided however that the substitution does not 10 abolish the native KIM protein's biological activity, ligand- or receptor-binding characteristics, or other functional property of interest. Exemplary non-conservative substitutions are those in which: (I) a hydrophilic residue, e.g., serine or threonine, is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine, or alanine; (ii) a cysteine residue is substituted for (or by) any other residue; (iii) a residue 15 having an electropositive side chain, e.g., lysine, arginine or histidine, is substituted for (or by) a residue having an electronegative charge, e.g., glutamic acid or aspartic acid; or (iv) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having such a side chain, e.g., glycine.

- Other KIM variants of this invention include truncation variants (comprising at 20 least a unique fragment of the corresponding KIM), insertion variants, and splice variants.

Other KIM variants within the invention are those with modifications which increase polypeptide stability. Such variants can contain, for example, one or more non-peptide bonds (which replace the peptide bonds) in the peptide sequence. Also included are: variants that include residues other than naturally occurring L-amino acids, such as D- 25 amino acids or non-naturally occurring or synthetic amino acids such as beta or gamma amino acids and cyclic variants. Incorporation of D- instead of L-amino acids into the polypeptide may increase its resistance to proteases. See, e.g., U.S. Patent 5,219,990.

KIM variants can be naturally-occurring, or produced through synthetic or molecular engineering techniques. Those of skill in the art will understand and appreciate that an engineered KIM variant can provide advantageous properties, e.g., in facilitating purification, improving stability, modulating a biological function, or the like. Thus, in 5 some instances, a KIM variant will be desired that lacks a glycosylation site, or that has decreased aggregation potential due to elimination of a hydrophobic surface, or that has improved folding efficiency due to elimination of a cysteine residue, or the like.

In general, KIM variants have at least fifty (50) % amino acid sequence homology or similarity with the corresponding KIM protein. Preferably, the variants have at least 10 sixty-five (65) % sequence similarity, more preferably at least eighty (80) % similarity with the corresponding KIM protein. Still more preferably, the sequence similarity is at least ninety (90) %, or most preferably, at least ninety-five (95) %. Other preferred KIM variants are those which 1) share at least forty (40) % similarity to the corresponding KIM protein, *and* 2) share at least eighty (80) % of aligned cysteine residues with the 15 corresponding KIM protein.

Just as it is possible to replace substituents of the amino acid backbone or scaffold, it is also possible to replace, modify or add non-amino acid moieties to the scaffold. Such moieties can occur naturally in a given KIM as a result of post-translational processing, including acetylation, methylation, phosphorylation, carboxylation or glycosylation. As 20 desired, such moieties can be removed or added by conventional synthetic or biochemical techniques. Further, non-natural moieties can be added to produce a derivative of a KIM or KIM variant of this invention. For example, polyethylene glycol (PEG) can be linked to a KIM to improve its stability or pharmacokinetic properties.

As will be readily appreciated, anti-KIM and anti-KIM variant antibodies can be 25 produced by conventional techniques. Specifically contemplated are polyclonal and monoclonal antibodies, including antigen-binding fragments thereof and engineered derivatives thereof. Antigen-binding fragments of intact antibodies include complete Fab fragments, F(ab')₂ compounds, V_H regions, and F_v regions. Engineered derivatives of antibodies of the invention include single chain antibodies (see, e.g., WO 96/23071), as

well as human, humanized, primatized, or chimeric antibodies (see, e.g., PCT/US 95/16709). Engineered derivatives of the present antibodies are produced, generally, using standard recombinant DNA techniques (Winter and Milstein, *Nature* 349: 293-99, 1991). These include "chimeric" antibodies, in which the antigen binding domain from an animal antibody is linked to a human constant domain. In this instance, an antibody with the desired KIM-binding selectivity is derived initially from a nonhuman mammal (e.g., a mouse, rat or hamster), and subjected to recombinant DNA manipulation to replace all or part of the hinge and constant regions of the heavy chain and/or the constant region of the light chain, with corresponding regions from a human immunoglobulin light chain or heavy chain. (See, e.g., Cabilly et al., United States Pat. No. 4,816,567; Morrison et al., *Proc. Natl. Acad. Sci.* 81: 6851-55, 1984). Chimeric antibodies reduce the immunogenic responses elicited by animal antibodies when used in human clinical treatments.

In addition, recombinant "humanized" antibodies can be synthesized. Humanized antibodies are antibodies initially derived from a nonhuman mammal in which recombinant DNA technology has been used to substitute some or all of the amino acids not required for antigen binding with amino acids from corresponding regions of a human immunoglobulin light or heavy chain. That is, they are chimeras comprising mostly human immunoglobulin sequences into which the regions responsible for specific antigen-binding have been inserted (see, e.g., PCT patent application WO 94/04679). Animals are immunized with the desired antigen, the corresponding antibodies are isolated and the portion of the variable region sequences responsible for specific antigen binding are removed. The animal-derived antigen binding regions are then cloned into the appropriate position of the human antibody genes in which the antigen binding regions have been deleted. Humanized antibodies minimize the use of heterologous (inter-species) sequences in antibodies for use in human therapies, and are less likely to elicit unwanted immune responses. Primatized antibodies can be produced similarly.

If desired, fully human antibodies with KIM-binding specificity which can be produced in nonhuman animals, such as transgenic animals harboring one or more human

immunoglobulin transgenes. Such animals may be used as a source for splenocytes for producing hybridomas, as is described in U.S. 5,569,825.

Identification of Specific KIMs of the Invention

To assess the dynamic biological processes of response to injury and tissue repair, a kidney ischemia-reperfusion model, which simulates acute renal failure, was employed. The results of studies in this model system now have been published, and appear in Ichimura et al. (1998), *J. Biol. Chem.* 273:4135-4142, the teachings of which are incorporated by reference herein. In this model, the kidney has the capacity for cell renewal (both structurally and functionally) after injury to tubular epithelial cells. The nephron is damaged functionally by an ischemic reperfusion injury that results in regional areas of proximal tubule cell death. During the repair process, the kidney proximal tubule epithelium undergoes a complex series of events including (1) cell death and cast formation in the tubule lumen (casts are aggregates of dead, semiviable and viable cells, as well as of cell debris); (2) proliferation of surviving proximal tubule epithelial cells; (3) formation of a poorly differentiated regenerative epithelium over the denuded basement membrane (this simplified epithelium expresses vimentin, a mesenchymal marker); and (4) differentiation of the regenerative epithelium to form fully functional proximal tubule epithelial cells. Gene expression analysis of the kidney at various timepoints following the onset of ischemia revealed the upregulation of many KIMs anticipated to be involved in the injury and repair/regeneration processes.

1. Generation of ischemic and normal rat adult kidneys

Ischemic injured rat kidneys are generated as described by Witzgall et al. (*J. Clin Invest.* 93: 2175-2188, 1994). Briefly, the renal artery and vein from one kidney of an adult Sprague-Dawley rat are clamped for 40 minutes and then reperfused. Injured kidneys are harvested from the rats at 24 hours and at 48 hours after reperfusion. Kidneys from sham-operated, normal adult Sprague-Dawley rats are also harvested.

2. mRNA isolation

Post-ischemic rat kidneys are prepared as described by Witzgall et al. (J. Clin. Invest. 93: 2175-2188, 1994). Briefly, the renal artery and vein of the left kidney of an adult Sprague Dawley rat are clamped for 40 minutes and then reperfused. The ischemic kidneys are removed from rats either 24 hours or 48 hours after reperfusion. Normal rat
5 kidneys are used as controls.

Total RNA is isolated with Trizol reagent (BRL catalog No. 1559-026). The kidney capsules are removed, then the kidneys are rinsed in PBS and immediately homogenized in Trizol solution. In some instances, the kidney is chopped into several pieces in PBS, frozen quickly in liquid nitrogen and kept at -70°C until it is processed for total RNA isolation.
10 The mRNA is purified from total RNA according to the manufacturer's instructions, using an mRNA purification kit (Pharmacia, Catalog No. 27-9258-02).

3(i). Representational difference analysis (RDA) method to clone short-fragment cDNAs up-regulated by ischemia

The RDA method of Hubank and Schatz (Nucleic Acid Research 22:5640-48, 15 1994) is performed as described, with modifications as follow. Double-stranded cDNA is synthesized using the Superscript Choice® system (BRL Catalog No. 18090), from mRNA isolated from rat kidney either 24 hours or 48 hours post-ischemia as a tester and normal rat kidney as a driver. The tester and driver cDNA is digested with DpnII and ligated to R-Bgl-12/24 oligonucleotides. The adapter-ligated cDNA is amplified by PCR, and the PCR product is digested with DpnII to remove the oligonucleotides. The tester cDNA is ligated
20 to J-Bgl-12-24 oligonucleotides.

Full length cDNA clones for Kim-1 and NMB contained in a plasmid vector are provided by T. Ichimura. They are digested with Sau3A1, purified and used as quenching reagents. cDNA fragments, 2-3 containing a fragment of annexin II, and 3-8 containing a 25 fragment of alpha 2 macroglobulin (both provided by T. Ichimura) are amplified by PCR with R-Bgl-24 primer, digested with DpnII to remove the oligonucleotides and used as quenching reagents. Tester cDNA is hybridized to an excess driver cDNA including the four quenching reagents described above. After mung bean nuclease digestion.

hybridization mixture is amplified by PCR to enrich the cDNA fragments upregulated by ischemia. Each of the PCR steps is tested with a range of template DNA concentrations, and the concentration giving the best signal is chosen for the next steps. The DNA mixture containing tester and driver DNA for the subtractive hybridization step is washed twice
5 with 70% EtOH by spinning for 3 minutes.

The second round cDNA subtraction is performed by hybridizing the first round cDNA subtraction product ligated to N-Bgl-12-24 oligonucleotides to an excess of the same driver cDNA used for the first round subtraction. The third round cDNA subtraction is performed by hybridizing the second round cDNA subtraction product ligated to J-Bgl-
10 12/24 oligonucleotides to an excess of the same driver cDNA used for the first round of cDNA subtraction at a ratio of 1:14,000. The final PCR product after the third round of subtraction is digested with DpnII to remove the oligonucleotides and ligated to pCR-Script SK(+) vector. This represents a selected cDNA library by RDA.

3(ii). Suppression subtractive hybridization (SSH) method to clone short-fragment cDNAs
15 up-regulated by ischemia

SSH is performed according to the manufacturer's instructions (Clontech, Catalog No. K1804-1) with certain modifications. Briefly, double-stranded cDNA are synthesized from mRNA isolated from rat kidney 24 hours or 48 hours post-ischemia as a tester, and from normal rat kidney as a driver with the Superscript Choice™ system for cDNA synthesis (BRL Catalog No. 18090). The cDNA is synthesized according to the manufacturer's instruction except that the first strand cDNA is synthesized at 42°C. cDNA is digested with RSAI. Tester cDNA after RSAI digestion is ligated to adaptors. For the first hybridization, tester cDNA with adaptors is hybridized with excess driver cDNA at 68°C for 12 hours. For the second hybridization, the mixture is hybridized at 68°C for 22
20 hours. The cDNA mixture after the second hybridization is initially amplified by PCR for 27 cycles only. Then, a portion of the PCR product is re-amplified for 10 or 13 cycles. The final subtracted PCR product is digested by RSAI to remove the adaptor, and separated on a gel. The three bands and the remaining smear are cut out separately and cloned to pCR-
25

Script SK (+) vector (Stratagene, Catalog No. 211188). This represents a selected cDNA library by SSH.

4. Isolation and Characterization of Subtracted Amplified cDNA Clones

Colonies are randomly picked from the selected RDA and SSH cDNA libraries, and plasmid DNA is isolated with Qiagen plasmid kit. Each cDNA clone, referred to as a Subtracted Amplified Clone (SAC) is sequenced with the vector primers. DNA sequences are checked against GeneBank/EMBL databases for homology by the program BLAST™.

Southern blots are prepared with the initial PCR products generated from normal and injured rat kidneys. The blots are hybridized to the inserts isolated from the SACs to confirm which SACs are induced by ischemia.

4. Isolation and Characterization of potential full length cDNA clones

4.25 ug of polyA+ mRNA isolated from rat kidney 24 hours post-ischemia, which has been purified twice by oligo dT chromatography, is used to generate a cDNA library. In order to obtain double-stranded cDNA with EcoRI adaptors, a Superscript Choice® system for cDNA synthesis (BRL Catalog No. 18090) is used following the supplier's protocol, except that the cDNA synthesis reaction is carried out at 42°C. The DNA is ethanol precipitated, washed, resuspended in 5 ul H2O, and ligated to 2 ug EcoRI digested and CIAP-treated Lambda ZAPII (Stratagene catalog No. 236612). The ligated DNA is packaged and used to infect E. coli XL-1 Blue MRF. The complexity of the library is 3.4×10^6 independent recombinant plaques. Another cDNA library is generated from 4 ug of polyA+ RNA from rat kidney 48 hours post-ischemia as described above.

The two cDNA libraries described above are screened with inserts from the SAC clones. pBluescript plasmid vector containing cDNA inserts are excised from Lambda ZAPII vector by in vivo excision. Inserts from the longest cDNA clones, referred to as Potential Full Length (PFL) clones, are sequenced. DNA sequences are checked by the program BLAST™ against the GenBank/EMBL databases for DNA homology. Predicted protein coding regions (open reading frames, or ORFs) from some of the PFL clones also were used to search the GenBank/EMBL databases.

Diagnostic Uses of the Compounds of the Invention

Anti-KIM antibodies of the invention, which specifically bind to a protein of the invention or a unique fragment thereof, are useful in several diagnostic methods. These agents can be labeled with detectable markers, such as fluoroscopically or radiographically opaque substances, and administered to an individual to allow imaging of tissues which express KIM protein. The agents can also be bound to (conjugated to) substances, such as horseradish peroxidase, which can be used as immunocytochemical stains to allow visualization of areas of KIM protein-positive cells on histological sections. A specific antibody could be used alone in this manner, and sites where it is bound can be visualized in a sandwich assay using an anti-immunoglobulin antibody which is itself bound to a detectable marker.

Specific antibodies to KIM protein are also useful in immunoassays to measure KIM presence or concentration in samples of body tissues and fluids. Such concentrations may be correlated with different disease states. As an embodiment of particular interest, the invention includes a method of diagnosing renal injury, or of monitoring a process of renal repair, by measuring the concentration of KIM or of KIM fragments in the urine, plasma or serum of a patient. Similarly, KIM can be measured in urine sediment, in particular in cellular debris in the urine sediment. Casts of renal tubule cells, which may be present in urine sediment from patients with ongoing renal disease, may contain elevated levels of KIM protein and mRNA.

Specific antibodies to KIM protein may also be bound to solid supports, such as beads or dishes, and used to remove the ligand from a solution, either for measurement, or for purification and characterization of the protein or its attributes (such as post-translational modifications). Such characterization of an individual's KIM protein is expected to be useful in identifying deleterious mutants or processing defects which interfere with KIM function and are associated with abnormal phenotypes. Each of these techniques is routine to those of skill in the immunological arts.

Additional imaging methods utilize KIM or KIM fragments, fused to imageable moieties, for diagnostic imaging of tissues that express KIM ligands, particularly tumors.

Further diagnostic techniques are based on demonstration of upregulated KIM mRNA in tissues, as an indication of injury-related processes. (See, e.g., PCT publication no. WO 97/44460).

Therapeutic Uses of the Compounds of the Invention

5 The therapeutic methods of the invention involve selectively promoting or inhibiting cellular responses that are dependent on the presence or concentration of any KIM, including without limitation KIM ligation, KIM enzyme activity, KIM secretion, KIM signalling, and KIM modulation of gene expression. In instances where a KIM and a KIM ligand are both membrane bound, and expressed by different cells, the signal transduction may occur in the KIM-expressing cell, in the KIM ligand-expressing cell, or 10 in both.

KIM ligation-triggered response in a KIM ligand-expressing cell may be generated by contacting the cell with exogenous KIM, KIM fusion proteins or activating antibodies against KIM ligand, either in vitro or in vivo. Further, responses of the KIM ligand-expressing cell that would otherwise be triggered by endogenous KIM could be blocked by 15 contacting the KIM ligand-expressing cell with a KIM ligand antagonist (e.g., an antagonist antibody that binds to KIM ligand), or by contacting the endogenous KIM with an anti-KIM antibody or other KIM-binding molecule which prevents the effective ligation of KIM with a KIM ligand.

20 Similarly, the responses triggered by KIM ligation in the KIM-expressing cell may be promoted or inhibited with exogenous compounds. For example, KIM ligation-triggered response in a KIM-expressing cell may be generated by contacting the cell with a soluble KIM ligand, or certain anti-KIM activating antibodies. Further, responses of the KIM-expressing cell that would otherwise be triggered by interaction with endogenous 25 KIM ligand could be blocked by contacting the KIM-expressing cell with an antagonist to KIM (e.g., a blocking antibody that binds to KIM in a manner that prevents effective, signal-generating KIM ligation), or by contacting the endogenous KIM ligand with an anti-

KIM ligand antibody or other KIM ligand-binding molecule which prevents the effective ligation of KIM with the KIM ligand.

Which of the interventions described above are useful for particular therapeutic uses depend on the relevant etiologic mechanism of either the pathologic process to be inhibited, or of the medically desirable process to be promoted, as is apparent to those of skill in the medical arts. For example, where KIM ligation results in desirable cellular growth, maintenance of differentiated phenotype, resistance to apoptosis induced by various insults, or other medically advantageous responses, one of the above-described interventions that promote ligation-triggered response may be employed. In the alternative, one of the inhibitory interventions may be useful where KIM ligation invokes undesirable consequences, such as neoplastic growth, deleterious loss of cellular function, susceptibility to apoptosis, or promotion of inflammation events.

Following are examples of the previously described therapeutic methods of the invention. One therapeutic use of the KIM-related compounds of the invention is for treating a subject with renal disease, promoting growth of new tissue in a subject, or promoting survival of damaged tissue in a subject, and includes the step of administering to the subject a therapeutically effective amount of a KIM protein of the invention, or of a pharmaceutical composition which includes a protein of the invention. The protein used in these methods can be a unique fragment of a full-length KIM protein, a soluble KIM variant or a soluble ligand thereof, a KIM fusion protein, or a KIM agonist. These methods can also be practiced by administering to the subject a therapeutically effective amount of an agonist antibody of the invention, or a pharmaceutical composition which includes an agonist antibody of the invention. A KIM protein can be administered concurrently with a therapeutically effective amount of a second compound which exerts a medically desirable adjunct effect. While tissues of interest for these methods include any tissue, preferred tissues include renal tissue, liver, neural tissue, heart, stomach, small intestine, spinal cord, or lung. Particular renal conditions which are expected to be beneficially treated with the compounds of the invention include acute renal failure, acute nephritis, chronic renal failure, nephrotic syndrome, renal tubule defects, kidney

transplants, toxic injury, hypoxic injury, and trauma. Renal tubule defects include those of either hereditary or acquired nature, such as polycystic renal disease, medullary cystic disease, and medullary sponge kidney. This list is not limited, and may include many other renal disorders (see, e.g., Harrison's Principles of Internal Medicine, 13th ed., 1994, which is herein incorporated by reference.) The subject of the methods may be human.

A therapeutic intervention for inhibiting growth of undesirable, KIM- or KIM-ligand-expressing tissue in a subject includes the step of administering to the subject a therapeutically effective amount of a KIM antagonist (e.g., an antibody blocks KIM ligation). In an embodiment of interest, the KIM antagonist or anti-KIM antibody can be used therapeutically to inhibit or block growth of tumors which depend on KIM protein for growth.

Other methods of the invention include killing KIM ligand-expressing tumor cells, or inhibiting their growth, by contacting the cells with a fusion protein of a KIM and a toxin or radionuclide, or an anti-KIM ligand antibody conjugated to a toxin or radionuclide. The cell can be within a subject, and the protein or the conjugated antibody is administered to the subject.

Also encompassed within the invention is a method for targeting a toxin or radionuclide to a cell expressing a KIM, comprising contacting the cell with a fusion protein comprising a KIM ligand and a toxin or radionuclide, or an anti-KIM antibody conjugated to a toxin or radionuclide. Another embodiment includes the method of suppressing growth of a tumor cell which expresses KIM, comprising contacting the cell with a fusion protein of KIM ligand and a toxin or radionuclide or with an anti-KIM antibody conjugated to a toxin or radionuclide; the cell may be within a subject, and the protein administered to the subject.

The term "subject" as used herein is taken to mean any mammal to which KIM can be administered. Subjects specifically intended for treatment with the method of the invention include humans, as well as nonhuman primates, sheep, horses, cattle, goats, pigs, dogs, cats, rabbits, guinea pigs, hamsters, gerbils, rats and mice.

Use of Compounds of the Invention in Gene Therapy

The KIM genes of the invention are introduced into damaged tissue, or into tissue where stimulated growth is desirable. Such gene therapy stimulates production of KIM protein by the transfected or transformed cells, promoting cell growth and/or survival of 5 cells that express the KIM protein.

In a specific embodiment of a gene therapy method, a gene coding for a KIM protein is introduced into a renal target tissue. The KIM protein is expected to be stably expressed and stimulate tissue growth, division, or differentiation, or to potentiate cell survival. Furthermore, a KIM gene can be introduced into a target cell using a variety of 10 well-known methods that use either viral or non-viral based strategies.

Once introduced into a target cell, sequences of interest can be identified by conventional methods such as nucleic acid hybridization using probes comprising sequences that are homologous/complementary to the inserted gene sequences of the vector. In another approach, the sequence(s) may be identified by the presence or absence 15 of a "marker" gene function (e.g., thymidine kinase activity, antibiotic resistance, and the like) caused by introduction of the expression vector into the target cell.

Formulation

In general, compounds of the invention are suspended, dissolved or dispersed in a pharmaceutically acceptable carrier or excipient. The resulting therapeutic composition 20 does not adversely affect the subject's homeostasis, particularly electrolyte balance. Thus, an exemplary carrier comprises normal physiologic saline (0.15M NaCl, pH 7.0 to 7.4). Other acceptable carriers are well known in the art and are described, for example, in Remington's Pharmaceutical Sciences, Gennaro, ed., Mack Publishing Co., 1990.

Acceptable carriers can include biocompatible, inert or bioabsorbable salts, buffering 25 agents, oligo- or polysaccharides, polymers, viscosity-improving agents, preservatives, and the like. In some embodiments, the term "carrier" encompasses liposomes and the HIV-1 tat protein (See Chen et al., Anal. Biochem. 227: 168-175, 1995) as well as any plasmid and viral expression vectors.

Any KIM compound of this invention can be used in the form of a pharmaceutically acceptable salt. Suitable acids and bases which are capable of forming salts with the polypeptides, nucleic acids and vectors of the present invention are well known to those of skill in the art, and include inorganic and organic acids and bases.

5 KIM compounds of the invention are dispersed in the carrier to concentrations sufficient to deliver to the subject a therapeutically effective amount of the compound, which is an amount sufficient to produce a detectable, preferably medically beneficial effect in the subject. Medically beneficial effects would include preventing, delaying or attenuating deterioration of, or detectably improving, the subject's medical condition. It is
10 expected that the concentration or amount of a KIM compound that will produce a medically beneficial effect will vary considerably with the circumstances in which the invention is practiced. An effective amount can be determined by an ordinarily skilled physician or other practitioner through no more than routine experimentation. As an example, an indication of the status of renal injury or renal function can be monitored with
15 one or more routine laboratory tests which measure the concentrations of relevant substances in blood or urine, other urine characteristics, or the rate of clearance of various substances from the blood into the urine. The parameters measured by these tests, either individually or in combination, can be used by a physician to assess renal function or damage. Examples of such parameters include the blood concentration of urea, creatinine
20 or protein; the urine concentration of protein or of various blood cells such as erythrocytes or leucocytes; urine specific gravity; amount of urine; the clearance rates of inulin, creatinine, urea or ρ -aminohippuric acid; and the presence of hypertension or edema.

In some embodiments, a KIM compound is formulated in a liposome delivery system, including without limitation any of a variety of unilamellar vesicles, multilamellar
25 vesicles, or stable plurilamellar vesicles, all of which can be prepared and administered according to methods well known to those of skill in the art, for example in accordance with the teachings of United States Patent 5,169,637, 4,762,915, 5,000,958 or 5,185,154. In addition, it may be desirable to express the novel polypeptides of this invention, as well as other selected polypeptides, as lipoproteins, in order to enhance their binding to

liposomes. As an example, treatment of human acute renal failure with liposome-encapsulated KIM protein may be performed *in vivo* by introducing a KIM protein into cells in need of such treatment using liposomes. The liposomes can be delivered via catheter to the renal artery. The recombinant KIM protein is purified, for example, from CHO cells by immunoaffinity chromatography or any other convenient method, then mixed with liposomes and incorporated into them at high efficiency. The encapsulated protein may be tested *in vitro* for any effect on stimulating cell growth.

Routes of Administration

The compounds of the invention may be administered in any manner which is medically acceptable. Depending on the specific circumstances, local or systemic administration may be desirable. Preferably, the compound is administered via a parenteral route such as by an intravascular, intravenous, intraarterial, subcutaneous, intramuscular, intratumor, intraorbital, intraventricular, intraperitoneal, subcapsular, intracranial, intraspinal, or intranasal injection, infusion or inhalation. The compound also may be administered by implantation of an infusion pump, or a biocompatible or bioerodable sustained release implant, or by installation of a catheter (e.g., in a renal artery), into the subject. Alternatively, certain compounds of the invention, or formulations thereof, may be appropriate for oral or enteral administration. Still other compounds of the invention will be suitable for topical administration.

Treatment Regimes

Determining appropriate dosage and frequency of treatment with any particular KIM compound to be administered to an individual is within the skills and clinical judgement of ordinary practitioners. The general dosage and treatment schedule is established by preclinical and clinical trials, which involve extensive but routine studies to determine the optimal administration parameters of the compound. Even after such recommendations are made, the practitioner will often vary these dosages for different individuals based on a variety of considerations, such as the individual's age, medical status, weight, sex, and concurrent treatment with other pharmaceuticals. Determining the

optimal dosage and administration regime for each KIM compound is a routine matter for those of skill in the pharmaceutical and medical arts.

Equivalents

- The invention may be embodied in other specific forms without departing from the spirit or essential characteristics thereof. The foregoing embodiments are therefore to be considered in all respects illustrative of, rather than limiting on, the invention disclosed herein. Scope of the invention thus is indicated by the appended claims rather than by the foregoing description, and all changes which come within the meaning and range of equivalency of the claims are intended to be embraced therein.
- 5

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Sanicola-Nadel, Michele
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Wei, Henry
Cate, Richard L

(ii) TITLE OF INVENTION: MODULATORS OF TISSUE REGENERATION

(iii) NUMBER OF SEQUENCES: 112

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Patent Administrator, Biogen, Inc.
(B) STREET: 14 Cambridge Center
(C) CITY: Cambridge
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02142

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/047,490
(B) FILING DATE: 23-MAY-1997

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/047,491
(B) FILING DATE: 23-MAY-1997

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2058 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HW010

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 8..646

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: complement (1618..1885)

(D) OTHER INFORMATION: /label= SAC_23807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCGACA GCT CGG ATC CCC CCA TCA CCT ACC TCA CAG ACT GCT CAG ACA Ala Arg Ile Pro Pro Ser Pro Thr Ser Gln Thr Ala Gln Thr 1 5 10	49
GAA GGT AGT AGG ATC ACA TCC AAA ATG CCT GTG GCG TCT ACC CAG GGG Glu Gly Ser Arg Ile Thr Ser Lys Met Pro Val Ala Ser Thr Gln Gly 15 20 25 30	97
TCC TCT CCC CCT ACC CCG GCT CTG TGG GCA ACC TCC CCC AGG GCT GCC Ser Ser Pro Pro Thr Pro Ala Leu Trp Ala Thr Ser Pro Arg Ala Ala 35 40 45	145
ACC CTA CCT CCC AAG TCC TCC ACC GGC ACA TCC TGT GAA CCA AAA Thr Leu Pro Pro Lys Ser Ser Ser Thr Gly Thr Ser Cys Glu Pro Lys 50 55 60	193
ATG GTC ATC AAC ACG GTC CCA CAG CTC CAC TCG GAG AAG ACA GTG TAT Met Val Ile Asn Thr Val Pro Gln Leu His Ser Glu Lys Thr Val Tyr 65 70 75	241
CTC AAG TCC AGT GAC AAC CGC CTG CTC ATG TCT CTC CTC CTC TTC CTC Leu Lys Ser Ser Asp Asn Arg Leu Leu Met Ser Leu Leu Leu Phe Leu 80 85 90	289
TTT GTC CTC TTC CTC TGC CTC TTT TCC TAC AAC TGC TAC AAG GGC TAC Phe Val Leu Phe Leu Cys Leu Phe Ser Tyr Asn Cys Tyr Lys Gly Tyr 95 100 105 110	337
CTG CCC GGA CAG TGC TTA AAG TTC CGC TCA GCC CTG CTG CTC GCA AAG Leu Pro Gly Gln Cys Leu Lys Phe Arg Ser Ala Leu Leu Leu Ala Lys 115 120 125	385
AAA AAA CCT AAG TCA GAG TTC TCT GAC CTG GAG CAG AGT GTG AAG GAG Lys Lys Pro Lys Ser Glu Phe Ser Asp Leu Glu Gln Ser Val Lys Glu 130 135 140	433
ACG CTG GTA GAA CCT GGG AGC TTC TCG CAG CAG AAC GGC GAC CAG CCC Thr Leu Val Glu Pro Gly Ser Phe Ser Gln Gln Asn Gly Asp Gln Pro 145 150 155	481
AAG CCA GCC TTG GAT ACC GGC TAT GAA ACC GAG CAG GAC ACT ATC ACC Lys Pro Ala Leu Asp Thr Gly Tyr Glu Thr Glu Gln Asp Thr Ile Thr 160 165 170	529
AGC AAG GTC CCC ACC GAT CGA GAG GAC TCG CAA CGT ATC GAC GAG CTC Ser Lys Val Pro Thr Asp Arg Glu Asp Ser Gln Arg Ile Asp Glu Leu 175 180 185 190	577

TCC GCC AGG GAC AAA CCG TTT GAT GTC AAG TGT GAA CTC AAG TTT GCA Ser Ala Arg Asp Lys Pro Phe Asp Val Lys Cys Glu Leu Lys Phe Ala 195 200 205	625
GAC TCG GAT GCC GAC GGG GAC TGAGGCCAGT GTGTCCCAGC CCGTGCCCCCT Asp Ser Asp Ala Asp Gly Asp 210	676
CCGTCTCGT GGAGAGTGT GTGTTGAACC TATTCACTAG CCGAGTCTTG TCACTGTGCA CCAGCCTCAG TCTTTGTCC CTTCTCTCT TGGGTTGAGC CTGTGACTTG TCCCCTTGT CCTTTGGGA AACAAAGTATC TATTCAAGCC TCAAGTCCCG GCAGTTGTTG GAGCGCTTAC TACACACCTG AGCCCTTGT GTCTGGGG AGAGATGGCC ACCTCCGTGG GCTGAGAAGA ACCACCCCTT CCTCTTCCGC TCCTCGAAGC AGCCACTGAG AGATAATTAA ATTCCAGATT GGAAATGACC TTTTGGTTT ATCAGATTGG TAACTTAATC CCCTGCCATC CGGGTGGCAC GGACGTTTTT CTTTCACTTC GTTATTTTT TTAGGATTTG CGCTCCTACT GTGTTGATGT CTTAGGTCAT TTTTTTTTTT TTAAGTTACC AGAGGAGATG TTTTGATATT CATGAGAAGA AGAACATTTT CTAGATTTT TTTTTTTTG GTTACATATT GAGATAAAAT ATGCCTCTGT TGCTTAAGAT TCTCAGGGAT AGACGTGATT TTTGCTAATT TCTTCCTGC TGTCGGAAC GTAGGCCTAA AACTGCTCT TGAGCTCACA CACTCACCCCT TTCCCTTTGG TGGGTTTTT TTTTTTTTG TTTTGTTTA TTAATCTTAC TCATTTGAA GGATTTCTT TATGAGCTTT TGTGTTGTT TTGTTTGT TTTTGT TCTCTTTTC CTGCCGTACA TCATCTACGA GGTGCCTTT GAGTGAGGGC AGATGGCCA GTGGCTTCGG GTGGCCAGT GGCTGTGGT GGCAGTTGAG CTGGCTCTGT GAGGGGAGGA GGGCTTAGAC GCCACGGCCC TGCTGCTCT CGGCACCTCC TGTCCCGATG GGTGGCGTCT TCATGAGGAT TACATCCTGT CTCTGCTGG TTCCATCTCG CACCTCTGCC CTTGGACTTC CACCTGACT GTCCACAAAA GACAGAAATG GGCTGGCTAG TTGGGCTCCC GCCCTCGGAC GGTGGCCGCA ACGTCCCGTG TGGGCGGCTG CCGCTGCAGC CTGACTCCTG CCGGTGTCTT TCAGGATGTG AACGGGTGGT ACGAATCTT ACATTTGTTT CTCACTCCT GTGTATGAAA CGACACTCAT TCCATGTAGA GGGTGACGGA CTCTGGATCC CCCCCCTTGT CGTGTAGACA CTCATCTCA GCGTGACCTG GTCCTGCCAT TCGGTGTAAA CATTGTGTT TATAAGATTT ACTTTGTTTT TATTTTCTA CTTGGAAC TG TACATATTTG AAAAAGTACC CAAATAAACC AGAAGCTTA TCGTTGAAAA AAAAAGTCG AC	1216 1276 1336 1396 1456 1516 1576 1636 1696 1756 1816 1876 1936 1996 2056 2058

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 amino acids
 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala Arg Ile Pro Pro Ser Pro Thr Ser Gln Thr Ala Gln Thr Glu Gly
 1 5 10 15

Ser Arg Ile Thr Ser Lys Met Pro Val Ala Ser Thr Gln Gly Ser Ser
 20 25 30

Pro Pro Thr Pro Ala Leu Trp Ala Thr Ser Pro Arg Ala Ala Thr Leu
 35 40 45

Pro Pro Lys Ser Ser Ser Thr Gly Thr Ser Cys Glu Pro Lys Met Val
 50 55 60

Ile Asn Thr Val Pro Gln Leu His Ser Glu Lys Thr Val Tyr Leu Lys
 65 70 75 80

Ser Ser Asp Asn Arg Leu Leu Met Ser Leu Leu Leu Phe Leu Phe Val
 85 90 95

Leu Phe Leu Cys Leu Phe Ser Tyr Asn Cys Tyr Lys Gly Tyr Leu Pro
 100 105 110

Gly Gln Cys Leu Lys Phe Arg Ser Ala Leu Leu Ala Lys Lys Lys
 115 120 125

Pro Lys Ser Glu Phe Ser Asp Leu Glu Gln Ser Val Lys Glu Thr Leu
 130 135 140

Val Glu Pro Gly Ser Phe Ser Gln Gln Asn Gly Asp Gln Pro Lys Pro
 145 150 155 160

Ala Leu Asp Thr Gly Tyr Glu Thr Glu Gln Asp Thr Ile Thr Ser Lys
 165 170 175

Val Pro Thr Asp Arg Glu Asp Ser Gln Arg Ile Asp Glu Leu Ser Ala
 180 185 190

Arg Asp Lys Pro Phe Asp Val Lys Cys Glu Leu Lys Phe Ala Asp Ser
 195 200 205

Asp Ala Asp Gly Asp
 210

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1727 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HW011

(xi) SEQUENCE DESCRIPTION: SEQ_ID NO:3:

GTCGACATGA TTGCTAGTGG TTCTGCTGGC TGTGAGGGCT CCCTGTCTGT GAGATCTTGT	60
TCGGGCTTTTC CACATCCAGG ATCCATCCAT TCACCCCTCA CCCACTCACC CTGTGGAGCA	120
TAAAACCTTT GCAGTCAGCC AGCATGGCAG AATGTCTATG CCTTGCTTCA GTTTCCAGGG	180
TAACTAAGCA TGTTTAATC CCACTGCCCT ACCCACTATT GCTCATTCTG TCTAGTCTTC	240
TGCTACCCAG CTTGTGTGGC TCCGTTCCCTG TCACGCCTTC AGACGTCACT GTTCTGTGAC	300
AGCGGTCTCT TTCCCCCTCTG CTCCACCCAT TCTGAGCTCT GGGATAGTCC TAAGCCCTGC	360
CCAGAGTAGG TGGACTGGTC GTTCCATGTC CGTGCTTGTG GGAGTTGTGG GGGTCTGTGG	420
CATCTGCTAA GGAGGTTTAT CCTCACGTCA CGGAATCCGG CAAGATGCGC CATGGTCTAC	480
ACTGCTTTCT CGAGCAGCGG CGAGAAAGGC CAGGATAACA CACGCCCTCTC TGCCCTGAGA	540
TAACAAACTG TCTGAGAAAG GAAGTGGCCC GTGTCTGGAA CATTGGCCCC AGTAAAGCAG	600
AGGAGACACT GCCATGTTTC CGTCATTCTG TTTCACTGCC TTGCTCTGGG GCTCAGGGGT	660
TGAAGAACATGA GGATACACCA TTGACCTTC AGGCCTTCCT CAGACCCCTCT TACAAAGCCT	720
GTTGTTGTGA GTCCAGCTCA TCAGCATGGC CGCCTTGTTC ACAGTTAGC ACCAGTGTCT	780
GCAACCGTGT CTGAAACGTA GCAGATGTCC AGTACTTTTT GTAAATGAAA AAATGAACAG	840
AGTGAAGAGA AAGAGTCACC ATGAAATTAA CTAGTCCAGT GAGCTGACCG TAGGGGCAGT	900
ATAAACATCC CCCAGCTCTT AATGTTCTGT CCTCAAGCTG TCCCCCTCCA CCTCTCCGCT	960
GGCAGGAGAG TGCTCTGTAT ATGTGGACAG TCGTTGAATG GCAGGTCCAG GATGTCCTCT	1020
GCAGGTGGAC AAAAGAGAAT TCTGCTTCCC GGAAGTCTCC TTTGCTGGTG ATCTCCATGT	1080
CCATCCTCAC TGAGCACTAG AATTAAAACC ACTCAATAAT GTGATATGTG TGGTCACCTT	1140
CAGTCAGTA GCAGTATTTC CTGGTCATTA ATATTCTGCA TTTTATTATG GTAAGATAGT	1200
ATAAGAAAAT GGTGGGCTGG TATATAGCCA GCCATGAGAC CACTCCTTAC GTCAAGGACT	1260
GGCAGAGTCT GAGGGACCTG AGTCTGGTC CTCCTCCTGT CCCCTCCTCC TGTAGCTATG	1320
GTGGCCTTCA GTATTCTGAG ACTGAAGGCT ACTACTTCAG GACACCTACT TGATCTTAGT	1380
ACTCTCAGAA CAGCTCTCCT CAGTTCTAGC TGTGATCGCG GGCTGCCTTT GGAACGTTAA	1440
CGTACTAATG GGTTAACGAC TTTCAGAAAG TGATTTAAA ACAAAATGAC TGGAAGTTTT	1500
GTCTGATAAA GCAAGTAGAA TGGAAATGTCT CAGACTGTCT CGTCACATTT TCATGTTCA	1560
TACGAAAAGA AAAGATTGAT AACCTATCTT TAGAAATAGT AATGTTAGTT CTTTCCTATT	1620
TTGTTAACAC CTTGAAGAAG GTTTTATTTA ACTCGTGAAC TTGTTCCCTT GTTATGACAT	1680
GATTGTTCCA GATTGAGGG ACAAAATAAA ATTAACCTTT CTAAAAAA	1727

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1060 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HW012

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 39..671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTCGACGCAT	GGGTGCAGGT	GACAAATGAG	CTGAAGAA	ATG ATC CCC AGA GGA	53
				Met Ile Pro Arg Gly	
				1 5	
ATA GGA TTG TGG CTG CCT TCA GCT CTG CTC CTC TCT CGG GTC CCA GGC					101
Ile Gly Leu Trp Leu Pro Ser Ala Leu Leu Leu Sér Arg Val Pro Gly					
10 15 20					
TGT TTC CCT CTG CGT GGC CCC AGC AGT GTG ACA GGC ACT GTG GGG GAG					149
Cys Phe Pro Leu Arg Gly Pro Ser Ser Val Thr Gly Thr Val Gly Glu					
25 30 35					
TCC CTG AGC GTG ACT TGT CAG TAT GAG GAG AGA TTC AAG ATG AAT AAG					197
Ser Leu Ser Val Thr Cys Gln Tyr Glu Glu Arg Phe Lys Met Asn Lys					
40 45 50					
AAA TAC TGG TGC AGA GGG TCA CAT GTT CTA CTT TGC AAA GAT ATT GTC					245
Lys Tyr Trp Cys Arg Gly Ser His Val Leu Leu Cys Lys Asp Ile Val					
55 60 65					
AAG ACC GGA GGC TCA GAA GAA GCT AGA AAT GGC CGA GTG TCC ATC AGG					293
Lys Thr Gly Gly Ser Glu Glu Ala Arg Asn Gly Arg Val Ser Ile Arg					
70 75 80 85					
GAT GAT CCA GAC AAC CTG ACC TTC ACA GTG ACC TTG GAG AGC CTC ATC					341
Asp Asp Pro Asp Asn Leu Thr Phe Thr Val Thr Leu Glu Ser Leu Ile					
90 95 100					
CTG GAG GAT GCA GGC ACC TAC ATG TGT GGG GTG GAT ATA CCA TTT ACT					389
Leu Glu Asp Ala Gly Thr Tyr Met Cys Gly Val Asp Ile Pro Phe Thr					
105 110 115					
AAT CAC CCC TTG GGG ATT GAT GAG TTC TTC AAG GTT GAA TTG TCT GTG					437
Asn His Pro Leu Gly Ile Asp Glu Phe Phe Lys Val Glu Leu Ser Val					
120 125 130					
GTC CCA GGT TCA AGC CTT TGG AGC AGT ACA ACA GTC CCA GAG ACC ATC					485
Val Pro Gly Ser Ser Leu Trp Ser Ser Thr Thr Val Pro Glu Thr Ile					
135 140 145					

AGA TCC TCA CTG GTT CAT ACT CAG CCC AGT GTG ACC ACA GAA GAC ACA	533
Arg Ser Ser Leu Val His Thr Gln Pro Ser Val Thr Thr Glu Asp Thr	
150 155 160 165	
ATT CCT GCT CCT AGT GCA CGG CCT CGG TCT CTT CTG GGC AGC CTC TAC	581
Ile Pro Ala Pro Ser Ala Arg Pro Arg Ser Leu Leu Gly Ser Leu Tyr	
170 175 180	
CTC TGC ATC CTG GTG TTT CTG GAG TTG CCC CTG TTC CTG TGC ATG CTC	629
Leu Cys Ile Leu Val Phe Leu Glu Leu Pro Leu Phe Leu Cys Met Leu	
185 190 195	
TGT GCC GTC CTG TGG GTG AAC AGG CCT CAG AGG TGC AGT GGG	671
Cys Ala Val Leu Trp Val Asn Arg Pro Gln Arg Cys Ser Gly	
200 205 210	
TGACATAGCA TTGGGCCCTG TCATGAGTAC CAGTGAAGTC TGTTGATATG GAGGCCCTGT	731
CCCTGGATGC ATCACCTCTG GTGGCCAAGG ACAACCAATA AAGCTGTGTT CTTGAGAATG	791
CTCTGAGACT TTTAGAACAT TCTCTGCACG TGTCAAACAC ATAAAAGAAT GTGCCAATA	851
AATACCAGCT GGGGAATTGG CTCAGCAGGT ACAACAATG GCTGCTTTTC CAGAGGTCC	911
GAGTTCAATT CCAATAACTA CATCGGTGGC TCACAACCAT CTCTAATGAG TTCAGATGCC	971
CTCTTCTGCT GTGCAGGTGC ACATTCACAT AGAATATTCA TACATTGAGT AAATTTATTA	1031
AAAGTAATTG CAGAATTAAA ACACAAAAA	1060

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 211 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ile Pro Arg Gly Ile Gly Leu Trp Leu Pro Ser Ala Leu Leu Leu	
1 5 10 15	
Ser Arg Val Pro Gly Cys Phe Pro Leu Arg Gly Pro Ser Ser Val Thr	
20 25 30	
Gly Thr Val Gly Glu Ser Leu Ser Val Thr Cys Gln Tyr Glu Glu Arg	
35 40 45	
Phe Lys Met Asn Lys Lys Tyr Trp Cys Arg Gly Ser His Val Leu Leu	
50 55 60	
Cys Lys Asp Ile Val Lys Thr Gly Gly Ser Glu Glu Ala Arg Asn Gly	
65 70 75 80	
Arg Val Ser Ile Arg Asp Asp Pro Asp Asn Leu Thr Phe Thr Val Thr	
85 90 95	
Leu Glu Ser Leu Ile Leu Glu Asp Ala Gly Thr Tyr Met Cys Gly Val	
100 105 110	

Asp Ile Pro Phe Thr Asn His Pro Leu Gly Ile Asp Glu Phe Phe Lys
 115 120 125
 Val Glu Leu Ser Val Val Pro Gly Ser Ser Leu Trp Ser Ser Thr Thr
 130 135 140
 Val Pro Glu Thr Ile Arg Ser Ser Leu Val His Thr Gln Pro Ser Val
 145 150 155 160
 Thr Thr Glu Asp Thr Ile Pro Ala Pro Ser Ala Arg Pro Arg Ser Leu
 165 170 175
 Leu Gly Ser Leu Tyr Leu Cys Ile Leu Val Phe Leu Glu Leu Pro Leu
 180 185 190
 Phe Leu Cys Met Leu Cys Ala Val Leu Trp Val Asn Arg Pro Gln Arg
 195 200 205
 Cys Ser Gly
 210

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3385 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HW013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTCGACTTTT TTTAACAAAG ATGATTAAAT ATTAAATATC ATACCCAGAA AAATCAAACA	60
ACTTCCAGAA TCAGACAGGT AAGATTCCCT AGTATGTTT TACCAAAATT TTATAAGATT	120
ATCTTAAATT TGAAGAATTG TGCATAAATA ACACAGGATA CCAAAGGAAA CTGAGCTGTA	180
TTTTTGCTT TGATGGAAA AAAAAAAA AAAACCTGAA ACCCAGAGAC ACTAACCAATT	240
TTGTGCACTG TATAACTCAT TGTGGAAGCT GAAACTTAGA ACTCATCTT GGAAATATAT	300
AATTGATGAA CCCACCTTTC CATTCAAGCTT TTAGGGTGAT GTAAAAGTGT ATGAATCCAC	360
TTACAAATAA ACTTAAAAGA CCTTTTCATG TTACCCATAC TCTTATCTTC TCAATGTATT	420
TCTATATGCT TACCTTTAGT AAGAGTACCA TGGAGTACTT TGATAGATGG AATGACAGAG	480
AAATGGATGT TTAAAGATCT TTAGGATGAA AAGGATAATT TAAGAAGCAT ATTTAAGAAG	540
CATGCTGATA TTGAAAAGGT AGTATAGGCA AGTACAGTGC ACTTCCACAG ACTACTCATA	600
CCTTCTTGTC CATCAGAAAG TCTGAGTGGG TTAGTTACAG TAAGGTCATG TTGATCTGGG	660

TCTATGCACC TGTGCTGAGG TCAGAGGACA ACTTTCAGGA GTCTGTTCTG CCCTTCCGTG	720
TGGGTCTAA GTATGCAACT CAAAGGTTGT CTGTCAGGTT GATTCTGCC AGTCATGAAA	780
CCTTGAGAA GAGGAAAAGG TGAGGAAGA ACAGGAACAG GATCATAGAA GTGACTAAGC	840
CAGAACATGT CATATTGAG GAAACATCAA GAGGTGCCCTA TAATAGGTT CCGAGAATGA	900
AAAAAAAAAC CAGATAACTT TACTGTCTAT TCCAGCCAGT TTGACTTAGA GGCACTGGCA	960
AAGTAGGTAC AGACAGCTGA GGTAGAAAAT GTGGAACATT ACTGTGGCAA CTGCTGCATC	1020
TTCGGGTGTG GAAGTCACAC CAATTCCACT TTTGGTTGGC ACTTCCCATC TTCTAAGAGA	1080
GAACCTTAA TTGAGCGGCC GTGAAAGAACT TGATAAAATCT ACGCTGCTGT GTGTCTCTCA	1140
CCACCACCCCT ACCTACATAG ACACCCCCAT TTAGTTGTT CCTGAGAATC AGAACAGAGC	1200
ACTTACACGA GGTACGGAA GCTGTGATGC CTAGTGTAAAG AAGTTAGAAG ATGACTGAAC	1260
ACAGGAAGAG AGCGGGCTTC CAGTGGGATC TAAATCAAAT CAGCGAGGAT CACTGGAAAC	1320
TGAGCTGAAA CTCAACTAAG ATTTAGCTTG CAAACAATAG AGATGTTCA TTTTAAAACC	1380
ACAGCAGATT AACAGTATAG CTGGGAAACA ACCAAGTGTG CTTTCAAAT TTCAGTTCCA	1440
CTATATCTGA GCATGGTTAA AATAGGGGTG AGTCCTATTT CATGGCTTTT ATCTATTAAA	1500
TATTTGTAAA CGTGCTCAAG TTCCCATTTTC TTTAACCTA CAAAATTCA GCTTCTCACA	1560
CTGGGGCTGT AGTTCTTAA TAGTTTCTA ATTCTGAGC CATCTTAGA CTTCTGAAAA	1620
CCTCAACTTC AGTCTCTTCT CACATAGCCA ACTATGAGAA CCTCCAAAGC AGAATGCAGT	1680
TTTCCTTGTG CCTTTAGCAA CAAGGCACCT TTACAAAAGT GGTTCTCAGT GAATGAAATG	1740
AAAGCATGAT CTTACAGTGT GCGACACTTC AGTAGTGATG ACTTAAATAA GTTTAAAAT	1800
AAATAAAATT ACAGAACCTA GGGGAGGTGA AAAATGGAA ACATGAAACA GTAGACCATA	1860
CTGCAGCTCA CAAAACAAGC AGTAAAACA TATAAACTAC CTATAATAGC CTCATTATAA	1920
CATGCAAACA CACTAACTCT GTTACATACA GATTGGATGT ATATCTGAAG TTGTTTATAG	1980
ATACAATGGG TTTAAGTTGG TAATTAATAA ATAGTACTAC CTTAGAATGT GTTGTGCTTT	2040
TAAGTATTAT GAAAGCTCAA GAGCCAGGCA TCTTCCTCTT CAGAGCTGTG TCCTGTTACA	2100
TAATTACTGG CAAAGTTCTA AACAGTTCTT TACTAAATCA CAAAATGCAT ACAGCTAGTG	2160
CCATTGTCTC AAGTCTTTT AGAATAGAAA TGTCGATGTG AAGCTATAAT TTTATTTGG	2220
TTTTATGATC CTGCAAGGGT TAAGTTGTC TGATTCTTCC CAGGGTACTG ATAAGTTCTC	2280
TAACATACCG GAGTAAGAGA ACTGAAACAG GTTATTCCC TCATCCTCAG GAATCTGCTT	2340
GAATATGGAT CAGCATATAT TGGACTTAAT GCTGCTTTG GGGGCCTAAT AGCAAACAGT	2400
CTATTTGGC GAATTTGAA CGTGACACAA GCTCGAGTAG CATCTAGCTT GCCAATGGCT	2460
GTGATCCCCT TTTGACAGC AAACCTGTCC TACCATAGTT TTGTAAGTTT ACCTTGAGT	2520
ACAGGTATGT TTTATTCAT TATCATCCAA GCCTGCATTT ATGCATACTA TATACACTTA	2580

TATATACTTC ACTCAAAACT GAAGGATTAG AACCGAGTAG GTGTGAGCTT TAATGAAGTG	2640
TTTAGGGAAG ACCAAATCTA TTCAACAACT GATTCAAGCTT AGGTCTGCCA ACCAACCAAGT	2700
GAGTACATAT CCACAGCCGT CAGTCACACA CTTCCCTGAC CTGAAGCAGC ATTCCCAGTG	2760
CTGCCTTGT TTCTTGTAA TTTGCACATT ATATGCAAGT TTTCTCTTT TAAAAAGATG	2820
TTTTTATTAA GGTATGTGTT TTGTCTGACT GTACATTGC ACACCAGGTA GTGGTACTGG	2880
ACCCCATATA CTAGTTACAG ATAAGGGTGA GCTGCCACGT GGGTGCTGGT AATTGAACTC	2940
AGCACTTAGT GCCATTGCTC TTAATTGAGA TCTCTCTCCA GCCCTGTATG AAAGTTCTTT	3000
AAAGTATAAG TATGTTGTGG GAATACAACt CTGTAATCTC TGAAGTACTA TGTGCATTGC	3060
AGCATTAGC AAAATGAAAG ACATAGTGTc CCATGTGTCC TGAACATGTA TTGTTATGTG	3120
TTCTATATGC ATGACCCCTTC TTATTAAGG CAGATTGGGG AAAGGGGTCA ATTTTGTGTT	3180
TTCTCCTAAA TAATAATCCA AATTTCTGAG AATCCAGAGT CAAGATTTGT TTTCTGTTT	3240
ATCAGTATTT CCTATCCAAG GCCTTAATAC ATGCTAAGCA TGTATTACACA CCAAGCTACA	3300
GTCCATCCTC TATAATTATT CCTTGACAT GATATGCACC ATTTTGCTG TGTCACTGAA	3360
AATAAAATGT GAACCTTATG TCGAC	3385

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1779 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HW014

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 175..804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTGCGACCTGG AAAGAGCTGC AGTGTTCGCG CTTGGTAGCT GGTGGACCGG GCTCAGCACC	60
TTGGGCTGGC TTTGTGCCCC AGAGGCTCAC CGGAAAAAGA CTTTCTCAGC CCTCGGACTC	120
CAGAGAGAGA TACTTTCGT GCTCCCCAAC CTTGACTCCT GCAGAAGCTG AGCG ATG	177
Met 1	
GCG TCC ATG GGG CTG CAG GTG CTG GGA ATC TCC TTG GCC GTC CTG GGC	225
Ala Ser Met Gly Leu Gln Val Leu Gly Ile Ser Leu Ala Val Leu Gly	
5 10 15	

TGG TTA GGA GTC ATC CTG AGT TGT TCG CTC CCC ATG TGG CGG GTG ACC Trp Leu Gly Val Ile Leu Ser Cys Ser Leu Pro Met Trp Arg Val Thr 20 25 30	273
GCC TTC ATC GGC AGC AAC ATC GTC ACG GCG CAG ACG AGC TGG GAA GGC Ala Phe Ile Gly Ser Asn Ile Val Thr Ala Gln Thr Ser Trp Glu Gly 35 40 45	321
CTG TGG ATG AAC TGC GTG GTG CAG ACG ACC GGC CAG ATG CAG TGC AAG Leu Trp Met Asn Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys Lys 50 55 60 65	369
ATG TAC GAC TCG ATG CTG GCC CTG CCG CAG GAC CTG CAG GCC GCC CGA Met Tyr Asp Ser Met Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala Arg 70 75 80	417
GCC CTG ATG GTC ATC AGC ATC ATC GTG GGT GCT CTG GGG ATG CTT CTC Ala Leu Met Val Ile Ser Ile Ile Val Gly Ala Leu Gly Met Leu Leu 85 90 95	465
TCA GTC GTA GGG GGC AAG TGC ACC AAC TGC ATG GAG GAC GAG ACC GTC Ser Val Val Gly Gly Lys Cys Thr Asn Cys Met Glu Asp Glu Thr Val 100 105 110	513
AAG GCC AAG GTC ATG ATC ACA GCC GGA GCC GTG TTC ATC GTG GCA AGC Lys Ala Lys Val Met Ile Thr Ala Gly Ala Val Phe Ile Val Ala Ser 115 120 125	561
ATG CTG ATT ATG GTG CCT GTG TCC TGG ACG GCA CAC AAC GTC ATC CGC Met Leu Ile Met Val Pro Val Ser Trp Thr Ala His Asn Val Ile Arg 130 135 140 145	609
GAC TTC TAC AAC CCT CTG GTG GCT TCC GGG CAG AAA AGG GAG ATG GGG Asp Phe Tyr Asn Pro Leu Val Ala Ser Gly Gln Lys Arg Glu Met Gly 150 155 160	657
GCC TCG CTT TAC ATC GGC TGG GCG GCT TCT GGG CTG CTG CTC CTG GGA Ala Ser Leu Tyr Ile Gly Trp Ala Ala Ser Gly Leu Leu Leu Gly 165 170 175	705
GGA GGC CTC CTC TGC TGC AAT TGC CCA CCT CGC CGC AAC GAA AAG CCC Gly Gly Leu Leu Cys Cys Asn Cys Pro Pro Arg Arg Asn Glu Lys Pro 180 185 190	753
TAC TCC GCC AAG TAC TCC GCC GCC CGC TCT GTT CCC GCC AGC AAC TAT Tyr Ser Ala Lys Tyr Ser Ala Ala Arg Ser Val Pro Ala Ser Asn Tyr 195 200 205	801
GTG TAAGGTGGGC CACTCTCTGT CCACATTGCC TTTATTTCT TGGATTGAAC Val 210	854
TCATAACGGC CTGTGGCCCC TCACATTCTC CAGGACCTGA CCAGCTGTGG GCTACTGACT GCTTGCAAAC CCGGACTGTG CTAAGTTACT AGCGTGTAGC CCTTGGGGAC CCACCTGGCC CATCTGGACA CATCTCAAGG CTCCAGCGAG GATAGATGTA AAAATATTTC CTTGCTTGCA TCCAGATTGC TCATGGATAC GGGGCTGAAG GCAGAACGAG CTGTCTGGGT ACGACAGTGG AGGGGGAGCT GGGTCCCTGCT GGCGGGATA GCTCAGCTGT GACTTTGGTC TCTGGAGTGG	914 974 1034 1094 1154

ATGTCCTGGT CATGTTAGCA AACATTCACT GCCCTTCCTC AGTGCCTCG CTCTCTCGCC	1214
TCCACGTTAC TCCCGCGCTA CTCTTGCCGT TTCTCGCCCC CGTTTCTGAG CACACCAGGT	1274
CCTGCCTGGA GTCTTGGTGT CGAGGATGAC TGACTGAAGG GGCCTTGAG AGCTGATGGG	1334
TTCTGCCATG GACTCCTCCC GGTGATTAGC AATGACTGGG GCCTTACCCA CCCACCTACC	1394
CTCGTAATGA AGTTCTGTGG AGTGGCTGGA CAGGTTGAG GGAAGGGTGG AGGTGGTTA	1454
AACTGGTTG GGGAGTGCTA GGGCTGGGA CCCAGAACCA GCCCAGGGTG TCCCCACCCC	1514
TTTCCCATAAC GGTCTTGCTA AATGTTCTGA TCTCTGTATA CCCCTCCCT CTTCAGAAGG	1574
ACCCCTGGGTG GGCCCCTCTG AATTCCCTAC CCTTGTCCAT TTCAAGGACG CTGGCCAGTC	1634
TGTGGAAGGT ACGGGGGTCT GATGGCATTG CACCAGGGAG CCTCCTGGAC TCCCTTGCCT	1694
TCTCTGTGGT TTCTTGTTT GTAATTAAAG GTCTGTTCAC AGCTGTAATT ATTATTTCT	1754
ACAATAATG GCACCTGCAG TCGAC	1779

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 210 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Ser Met Gly Leu Gln Val Leu Gly Ile Ser Leu Ala Val Leu
 1 5 10 15

Gly Trp Leu Gly Val Ile Leu Ser Cys Ser Leu Pro Met Trp Arg Val
 20 25 30

Thr Ala Phe Ile Gly Ser Asn Ile Val Thr Ala Gln Thr Ser Trp Glu
 35 40 45

Gly Leu Trp Met Asn Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys
 50 55 60

Lys Met Tyr Asp Ser Met Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala
 65 70 75 80

Arg Ala Leu Met Val Ile Ser Ile Ile Val Gly Ala Leu Gly Met Leu
 85 90 95

Leu Ser Val Val Gly Gly Lys Cys Thr Asn Cys Met Glu Asp Glu Thr
 100 105 110

Val Lys Ala Lys Val Met Ile Thr Ala Gly Ala Val Phe Ile Val Ala
 115 120 125

Ser Met Leu Ile Met Val Pro Val Ser Trp Thr Ala His Asn Val Ile
 130 135 140

Arg Asp Phe Tyr Asn Pro Leu Val Ala Ser Gly Gln Lys Arg Glu Met
 145 150 155 160

Gly Ala Ser Leu Tyr Ile Gly Trp Ala Ala Ser Gly Leu Leu Leu
 165 170 175

Gly Gly Gly Leu Leu Cys Cys Asn Cys Pro Pro Arg Arg Asn Glu Lys
 180 185 190

Pro Tyr Ser Ala Lys Tyr Ser Ala Ala Arg Ser Val Pro Ala Ser Asn
 195 200 205

Tyr Val
 210

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2537 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (vii) IMMEDIATE SOURCE:

- (B) CLONE: HW015

- (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 11..2176
- (D) OTHER INFORMATION: /product= "predicted polypeptide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTGACCAAA ATG GCA GCC TTG GAA GAA GAA TTC ACG TTG TCT ACT GGA	49
Met Ala Ala Leu Glu Glu Glu Phe Thr Leu Ser Thr Gly	
1 5 10	
GTC TTA GGC GCC GGG CCT GAA GGA TTC CTA GGT GTA GAG CCC AGT GAC	97
Val Leu Gly Ala Gly Pro Glu Gly Phe Leu Gly Val Glu Pro Ser Asp	
15 20 25	
AAG GCC GAC CAG TTC CTA GTG ACC GAC AGA GGC AGG ACC GTC GTC CTC	145
Lys Ala Asp Gln Phe Leu Val Thr Asp Arg Gly Arg Thr Val Val Leu	
30 35 40 45	
TAC AAG GTT TCT GAC CAG AAA CCC TTG GGC AGC TGG TCG GTG AAA CAA	193
Tyr Lys Val Ser Asp Gln Lys Pro Leu Gly Ser Trp Ser Val Lys Gln	
50 55 60	
GGC CAG ACT ATA ACA TGT CCT GCT GTG TGC AAC TTT CAG ACT GGA GAG	241
Gly Gln Thr Ile Thr Cys Pro Ala Val Cys Asn Phe Gln Thr Gly Glu	
65 70 75	
TAT ATT ATG GTA CAT GAC CATT AAG GTT TTG AGA ATA TGG AAT AAT GAA	289
Tyr Ile Met Val His Asp His Lys Val Leu Arg Ile Trp Asn Asn Glu	
80 85 90	
GAC GTA AAC CTG GAT AAA GTA TTC AAA GCT ACA CTG TCA GCT GAG GTC	337
Asp Val Asn Leu Asp Lys Val Phe Lys Ala Thr Leu Ser Ala Glu Val	

95	100	105	
CAT AGG ATC CAC TCA GTA CAA AGA ACA GAA CCC CTG GTG CTG TTC CGA His Arg Ile His Ser Val Gln Arg Thr Glu Pro Leu Val Leu Phe Arg 110 115 120 125			385
AGA GGC GCT GCT CGT GGG TTA GAG GCC TTG CTT GCA GAG CCA CAG CAG Arg Gly Ala Ala Arg Gly Leu Ala Leu Leu Ala Glu Pro Gln Gln 130 135 140			433
AAC ATT GAA GCT GTC ATA CCA GAT GAG GAA GTG ATC GAG TGG TCA GAG Asn Ile Glu Ala Val Ile Pro Asp Glu Glu Val Ile Glu Trp Ser Glu 145 150 155			481
GTT TTC ATG TTA TTT AAG CAA CCG GTT TTA ATT TTT ATT ACT GAA AAT Val Phe Met Leu Phe Lys Gln Pro Val Leu Ile Phe Ile Thr Glu Asn 160 165 170			529
CAT GGG AGT TAT GTT GCT TAT GTA CAA TTG TGC AAA TCA CAC AGC TTA His Gly Ser Tyr Val Ala Tyr Val Gln Leu Cys Lys Ser His Ser Leu 175 180 185			577
AGC AAA TAC ATA CTC TTA CTT GGA AAA GAA GAA AAA TCT GCT AAA CCA Ser Lys Tyr Ile Leu Leu Gly Lys Glu Lys Ser Ala Lys Pro 190 195 200 205			625
AAT TTT ACT GCA CGT GTG GAT GGG AAA TTC ATC TCC CTG GTG TCG CTA Asn Phe Thr Ala Arg Val Asp Gly Lys Phe Ile Ser Leu Val Ser Leu 210 215 220			673
GGC TCT GAT GGG TGT GTA TAT GGA ACC TTG GTA CCA ATA TAT TCA AGT Gly Ser Asp Gly Cys Val Tyr Gly Thr Leu Val Pro Ile Tyr Ser Ser 225 230 235			721
GAC ACG GAA AAC AAT CAG AGG TTA GTT AGA GCA TTG ATG CTC AAG ACG Asp Thr Glu Asn Asn Gln Arg Leu Val Arg Ala Leu Met Leu Lys Thr 240 245 250			769
GTT GTG TCT GGC AGT GCT CGA AAT GGT TCT GCC CTC ACC ATC CTG GAT Val Val Ser Gly Ser Ala Arg Asn Gly Ser Ala Leu Thr Ile Leu Asp 255 260 265			817
CAA GAC CAC ATA GCA GTC CTG GGA CCT CCA CTT CCA GCT TCT AAG GAA Gln Asp His Ile Ala Val Leu Gly Pro Pro Leu Pro Ala Ser Lys Glu 270 275 280 285			865
TGC CTC TCC ATA TGG AAC ATA AAA TTT CAG ACA TTA CAG ACA TCA AAA Cys Leu Ser Ile Trp Asn Ile Lys Phe Gln Thr Leu Gln Thr Ser Lys 290 295 300			913
GAG CTG CCA CAA GGA ACC AGT GGG CAA CTC TGG TAT CAT GGG GAA ATA Glu Leu Pro Gln Gly Thr Ser Gly Gln Leu Trp Tyr His Gly Glu Ile 305 310 315			961
CTA TTT ATG CGA CAT GGG AAA AGT CTA ACT GTG ATT CCA TAC AAG TGC Leu Phe Met Arg His Gly Lys Ser Leu Thr Val Ile Pro Tyr Lys Cys 320 325 330			1009
GAA GCA TCA TCT CTG GCG AGC GCT CTT GGG AAG CTC AAG CAT ACT CAA Glu Ala Ser Ser Leu Ala Ser Ala Leu Gly Lys Leu Lys His Thr Gln 335 340 345			1057
GAG TCA GGC AGT CAT TCC GTG CCC CAT TTT GTA AAC TGG GAG ACG TGT			1105

Glu Ser Gly Ser His Ser Val Pro His Phe Val Asn Trp Glu Thr Cys				
350	355	360	365	
TCA GAA TAT GAA CTT GGG TCC TAC AGT GCA AAG CAG ACA AGA ACT CTT				1153
Ser Glu Tyr Glu Leu Gly Ser Tyr Ser Ala Lys Gln Thr Arg Thr Leu				
370	375	380		
AGA AAA AAA ACT GAA ACA AAT TTA CAC CCA GAA GTT CCA GGA GTC AAA				1201
Arg Lys Lys Thr Glu Thr Asn Leu His Pro Glu Val Pro Gly Val Lys				
385	390	395		
GAA CTT TTA TCA ATA ATA AAG AAA GAT TCA GAA AAG CAC ATT GAA GTA				1249
Glu Leu Leu Ser Ile Ile Lys Lys Asp Ser Glu Lys His Ile Glu Val				
400	405	410		
GAA CTA CGT AAG TTT TTG GCT AAG TCG ACA CCT GAC TTT CAT ACT ATA				1297
Glu Leu Arg Lys Phe Leu Ala Lys Ser Thr Pro Asp Phe His Thr Ile				
415	420	425		
ATT GGA GAC ATA GTG TCT GGA CTT CTG GGA AGA TGT AAA GTG GAA CCA				1345
Ile Gly Asp Ile Val Ser Gly Leu Leu Gly Arg Cys Lys Val Glu Pro				
430	435	440	445	
TCG TTT TAC CCC CGG AAC TGT CTG ATG CAG CTC ATC CAG ACA CAC GTG				1393
Ser Phe Tyr Pro Arg Asn Cys Leu Met Gln Leu Ile Gln Thr His Val				
450	455	460		
CTT TCC TAC AGC TTA TGC CCT GAC TTG ATG GAG ATT GCC CTA GAG CAC				1441
Leu Ser Tyr Ser Leu Cys Pro Asp Leu Met Glu Ile Ala Leu Glu His				
465	470	475		
ACA GAT GTG CAG ATG TTA CAG CTG TGT CTG CAG CAG TTC CCT GAC ATT				1489
Thr Asp Val Gln Met Leu Gln Leu Cys Leu Gln Gln Phe Pro Asp Ile				
480	485	490		
CCT GAG TCC ACC ACC TGT GCT TGC TTA AAA CTT TTC CTG AGC ATT GGT				1537
Pro Glu Ser Thr Thr Cys Ala Cys Leu Lys Leu Phe Leu Ser Ile Gly				
495	500	505		
GAT GAC TGT CTT CGG GAC AGT AAT GTC AGC ATG GAG TCA GTT TTT GAT				1585
Asp Asp Cys Leu Arg Asp Ser Asn Val Ser Met Glu Ser Val Phe Asp				
510	515	520	525	
TAT GGT GAT ACT ACA CAA GAT GAG AAA AAG GAA ATG GAA GAG CAA ACT				1633
Tyr Gly Asp Thr Thr Gln Asp Glu Lys Lys Glu Met Glu Glu Gln Thr				
530	535	540		
GAA ATT GTT CAG AAT GGC TTC GGT CCT GAA GAT GGT GGC TGC AGT AAA				1681
Glu Ile Val Gln Asn Gly Phe Gly Pro Glu Asp Gly Gly Cys Ser Lys				
545	550	555		
GAT AGT CAG CAG TTG AAC AAA AAG CCT GGT GAC ACA GCA CAG GAG CCC				1729
Asp Ser Gln Gln Leu Asn Lys Lys Pro Gly Asp Thr Ala Gln Glu Pro				
560	565	570		
ATC TCC TTC CCT GTG ACC TTG TGT CCT GTG GCA CCA AAG CGA GCA GCT				1777
Ile Ser Phe Pro Val Thr Leu Cys Pro Val Ala Pro Lys Arg Ala Ala				
575	580	585		
CTG CTA AAT GCA GTC CTT CAT TCA GCA TAC AGT GAG CCC TTC CTC CTG				1825
Leu Leu Asn Ala Val Leu His Ser Ala Tyr Ser Glu Pro Phe Leu Leu				
590	595	600	605	

CCG CAC TTG AAG GAC ATC CCT GCG AAG CAT ATA ACG CTG TTT CTG CAG Pro His Leu Lys Asp Ile Pro Ala Lys His Ile Thr Leu Phe Leu Gln 610 615 620	1873
TAT TTG TAT TTC CTC TAT TTG AAG TGC ACT GGC AGT GCT ACC ATG ACT Tyr Leu Tyr Phe Leu Tyr Leu Lys Cys Thr Gly Ser Ala Thr Met Thr 625 630 635	1921
CTC CCT GGA GTA AGC CCT CCA ACC GTG AGC CAG ATC ATG GAT TGG ATA Leu Pro Gly Val Ser Pro Pro Thr Val Ser Gln Ile Met Asp Trp Ile 640 645 650	1969
TGC CTA CTT CTA GAT GCT AAT TTT ACT GTC GTC TTA ATG ATA CCA GAA Cys Leu Leu Leu Asp Ala Asn Phe Thr Val Val Leu Met Ile Pro Glu 655 660 665	2017
GCA AAA AGA CTT TTG CTT AAT CTT TAC AAT TTT GTG AAA TCG CAG ATC Ala Lys Arg Leu Leu Asn Leu Tyr Asn Phe Val Lys Ser Gln Ile 670 675 680 685	2065
TCC ATC TAC TCC GAG CTC AAC AAG ATT GAA GTC AGC TTC CGG GAG CTG Ser Ile Tyr Ser Glu Leu Asn Lys Ile Glu Val Ser Phe Arg Glu Leu 690 695 700	2113
CAG AGG TTA AAT CAG GAG AAG AGC AGT AGA GGA CTG TAC TCC ATC GAA Gln Arg Leu Asn Gln Glu Lys Ser Arg Gly Leu Tyr Ser Ile Glu 705 710 715	2161
GTT CTG GAA CTT TTC TGACAGCCAG AGACAGTCCTT ACTGGTTGTC CTAGAACTGG Val Leu Glu Leu Phe 720	2216
ATATATAGAC CAAGCTGGCC TCAAACTCAC AGAGATCCAA CCCAGAGCAC TGCGATTAAA GGTGTGGCCA CCACACCTGG CTTAACGGAT TTTTTTATAT GAATGTACCT GTTCATCCAG GGGAGAAAGT TTTGTTGTA TCCATCTCAG TGTCCAGAGA GGAGTGTGAG TCTCTGCACC ATCACATACC ACCATTCCCTC AGTGCTACGG GTTCCACAGA CATCACTTCT GGGTTGCAGA CATCACTGGA AGAATGTTAC AAACTTTTA AACATGGAAT TGAGTTGATT TTAAGTAAAC TTATTTGTGT ACTGATAAAA A	2276 2336 2396 2456 2516 2537

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 722 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ala Ala Leu Glu Glu Glu Phe Thr Leu Ser Thr Gly Val Leu Gly
 1 5 10 15
 Ala Gly Pro Glu Gly Phe Leu Gly Val Glu Pro Ser Asp Lys Ala Asp
 20 25 30
 Gln Phe Leu Val Thr Asp Arg Gly Arg Thr Val Val Leu Tyr Lys Val

35	40	45
Ser Asp Gln Lys Pro Leu Gly Ser Trp Ser Val Lys Gln Gly Gln Thr		
50	55	60
Ile Thr Cys Pro Ala Val Cys Asn Phe Gln Thr Gly Glu Tyr Ile Met		
65	70	75
80		
Val His Asp His Lys Val Leu Arg Ile Trp Asn Asn Glu Asp Val Asn		
85	90	95
Leu Asp Lys Val Phe Lys Ala Thr Leu Ser Ala Glu Val His Arg Ile		
100	105	110
His Ser Val Gln Arg Thr Glu Pro Leu Val Leu Phe Arg Arg Gly Ala		
115	120	125
Ala Arg Gly Leu Glu Ala Leu Leu Ala Glu Pro Gln Gln Asn Ile Glu		
130	135	140
Ala Val Ile Pro Asp Glu Glu Val Ile Glu Trp Ser Glu Val Phe Met		
145	150	155
160		
Leu Phe Lys Gln Pro Val Leu Ile Phe Ile Thr Glu Asn His Gly Ser		
165	170	175
Tyr Val Ala Tyr Val Gln Leu Cys Lys Ser His Ser Leu Ser Lys Tyr		
180	185	190
Ile Leu Leu Leu Gly Lys Glu Glu Lys Ser Ala Lys Pro Asn Phe Thr		
195	200	205
Ala Arg Val Asp Gly Lys Phe Ile Ser Leu Val Ser Leu Gly Ser Asp		
210	215	220
Gly Cys Val Tyr Gly Thr Leu Val Pro Ile Tyr Ser Ser Asp Thr Glu		
225	230	235
240		
Asn Asn Gln Arg Leu Val Arg Ala Leu Met Leu Lys Thr Val Val Ser		
245	250	255
Gly Ser Ala Arg Asn Gly Ser Ala Leu Thr Ile Leu Asp Gln Asp His		
260	265	270
Ile Ala Val Leu Gly Pro Pro Leu Pro Ala Ser Lys Glu Cys Leu Ser		
275	280	285
Ile Trp Asn Ile Lys Phe Gln Thr Leu Gln Thr Ser Lys Glu Leu Pro		
290	295	300
Gln Gly Thr Ser Gly Gln Leu Trp Tyr His Gly Glu Ile Leu Phe Met		
305	310	315
320		
Arg His Gly Lys Ser Leu Thr Val Ile Pro Tyr Lys Cys Glu Ala Ser		
325	330	335
Ser Leu Ala Ser Ala Leu Gly Lys Leu Lys His Thr Gln Glu Ser Gly		
340	345	350
Ser His Ser Val Pro His Phe Val Asn Trp Glu Thr Cys Ser Glu Tyr		
355	360	365
Glu Leu Gly Ser Tyr Ser Ala Lys Gln Thr Arg Thr Leu Arg Lys Lys		

370

375

380

Thr Glu Thr Asn Leu His Pro Glu Val Pro Gly Val Lys Glu Leu Leu
 385 390 395 400

Ser Ile Ile Lys Lys Asp Ser Glu Lys His Ile Glu Val Glu Leu Arg
 405 410 415

Lys Phe Leu Ala Lys Ser Thr Pro Asp Phe His Thr Ile Ile Gly Asp
 420 425 430

Ile Val Ser Gly Leu Leu Gly Arg Cys Lys Val Glu Pro Ser Phe Tyr
 435 440 445

Pro Arg Asn Cys Leu Met Gln Leu Ile Gln Thr His Val Leu Ser Tyr
 450 455 460

Ser Leu Cys Pro Asp Leu Met Glu Ile Ala Leu Glu His Thr Asp Val
 465 470 475 480

Gln Met Leu Gln Leu Cys Leu Gln Gln Phe Pro Asp Ile Pro Glu Ser
 485 490 495

Thr Thr Cys Ala Cys Leu Lys Leu Phe Leu Ser Ile Gly Asp Asp Cys
 500 505 510

Leu Arg Asp Ser Asn Val Ser Met Glu Ser Val Phe Asp Tyr Gly Asp
 515 520 525

Thr Thr Gln Asp Glu Lys Lys Glu Met Glu Glu Gln Thr Glu Ile Val
 530 535 540

Gln Asn Gly Phe Gly Pro Glu Asp Gly Gly Cys Ser Lys Asp Ser Gln
 545 550 555 560

Gln Leu Asn Lys Pro Gly Asp Thr Ala Gln Glu Pro Ile Ser Phe
 565 570 575

Pro Val Thr Leu Cys Pro Val Ala Pro Lys Arg Ala Ala Leu Leu Asn
 580 585 590

Ala Val Leu His Ser Ala Tyr Ser Glu Pro Phe Leu Leu Pro His Leu
 595 600 605

Lys Asp Ile Pro Ala Lys His Ile Thr Leu Phe Leu Gln Tyr Leu Tyr
 610 615 620

Phe Leu Tyr Leu Lys Cys Thr Gly Ser Ala Thr Met Thr Leu Pro Gly
 625 630 635 640

Val Ser Pro Pro Thr Val Ser Gln Ile Met Asp Trp Ile Cys Leu Leu
 645 650 655

Leu Asp Ala Asn Phe Thr Val Val Leu Met Ile Pro Glu Ala Lys Arg
 660 665 670

Leu Leu Leu Asn Leu Tyr Asn Phe Val Lys Ser Gln Ile Ser Ile Tyr
 675 680 685

Ser Glu Leu Asn Lys Ile Glu Val Ser Phe Arg Glu Leu Gln Arg Leu
 690 695 700

Asn Gln Glu Lys Ser Ser Arg Gly Leu Tyr Ser Ile Glu Val Leu Glu

705

710

715

720

Leu Phe

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HW016

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 385..748
- (D) OTHER INFORMATION: /label= SAC_24530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATTATTCTCC CCTTGTCA	TTC	AAAAGAAATC AGCAAAACCA AACAACTGGC TACACCACGA	60
ATTGTCGTTA AATTGCTAA CTGGTGTCTA	AAAGCCGTGT AGCTACCTCG GTCCTGCTTG	120	
CTAGGTTGC CACTAGAAGG AAGCATACTT AAAACAATGG CTACTTGGAT CCTCAGGGAG	180		
ATCCTGTCTG CAGTCGCGTG GTCACCCCTTA GCTTCATCAA AGCACTAACAA GCTCACCCGG	240		
CCAGGCTTCA TGAGCACTGA CCCTCAAGCA AGCAGGTTTA TTAAACATTT AGATGCCAAC	300		
CTCACTTACT GTTTCCTGCA GTCATGGAGA GTTTACTTAA CAAGTTTGTA AATAATAAAC	360		
TGGCACTTG CACACAGACT TGGTACTATC CTAGGGGAAG GCCTGCTTTA TTTGGTTTCT	420		
AGACCGAGTA GGAAGTGATC CATTACAC TGAGGGCAGC CCCATTCAAGA GTCTTAAGTG	480		
ACTAAGCCAG TGTTGAACAA GCAATTCCA GGCTTGTTC TTCAGGGAAC TTCCCATCAG	540		
CTTTGAAGTC GGTCCCTGTGC ACCCTAGGCA CATGGATCAG TTCACTAAGTG GGGTTCAAGTG	600		
GAGAGAACTT CCCCTCTAGA AGTCACTTGA AACTTAGATG AGATTTGGGA CACTTGCTGG	660		
TTGACTCTGT CTCATTGTG TAAAAAGTAG TTTNTNTNAA NANTNGGTTT TNNTTTTTTT	720		
TTCAAGGTT TACTTGTCC CATTCTANG TTANTACAAA GTCTTGAAAG GGCCTTTGTA	780		
GGGCTTTTA ANNCAGGGTC TTAACTATGT AACTCTGGCT TGGCCTGGAA CTTGCTATGT	840		
AGACCAGGTT ACCCTCAAAC TTGCCTGTCT TCCCAAATAC TGGGATTAAG GTTTCTGTGA	900		
CCATACCTGG CTTTACCTGA TGAATTCTA AACACCAGAA AACCAAGTACT GTATGAGATG	960		

TTAATGTGTG TTCCTTCAG ACTGGAGTAC AGACCAGTAG ATAACAGATA ACAGCTGGTT	1020
CACCTTAATC TGCCTTTTG TGTATTAATC TGTGTTAGA GAACGGAACA ATAGCCAGAA	1080
TTNNNCTAGC GAGTCGAGG CCAGTTGGTG TATATGTGGG ACTCTTAACC AAAACAGCAA	1140
GCGTTCCCTG GGGTAGTCA CAATGATCTC CAGCTTCCTT GTTAACCAGA TAACTGCNAN	1200
TCCAGATGTA TGACCCCTGGT TGGTTTATTG TATTGATATG TTTCTGTAAT ATGAGTAAAT	1260
TATTGTTACT TAAAAGTAAT AAATTCAAGT TTCAAAATTG AAAAA	1305

(2) INFORMATION FOR SEQ ID NO:12;

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 955 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HW017

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 393..627
- (D) OTHER INFORMATION: /label= SAC_24091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTGCAACATC CTGTTATGAC AAGCCCGTCT CGATACTGAC AACTGAAGTG GAAATTGCTT	60
GAACATCAAG ATAGCTAACT CGGAAAGAAC CCCAGACTTT GGATAGTTTC TGAGTCTTCT	120
AGAATTTCC AAGAAGAAC CATGGTGGCA AATGCGGAGA CTCGGGCGGG CACTGGGAAC	180
ACAGCACAGT GGTCTTAGGG AGGTGCTTTG TCAGGAATGA ACAGTCATGG TTATAATCCA	240
CGTTTCCATT GCTACTCACG AATGATTCTC TTCTGTTTG TTTTAAAT TTTTTACAC	300
TGAATTCTA TTTAGACACT AAAACATATA GGGGTGCTTG TCACCCGGAT ACATTATCT	360
GTGAGCCAGC TATTCGGATG TCATGGCTGG GTACCTAACT TACTTCCATA TGTGAAGTGT	420
GCTAAACTCA AACCAGTTA CAGAAACGAT GTATTTGTG TATAGTAAAT TGTATATTCA	480
CCCTTTACC ACGGCCGGTT TTTTAAACAA ATGAATACTC TAGATTTTC TTCCAAATGA	540
GGTTACTGTT GGGGTGGGGT TGACTTAGTG ATGCTGTAGA AGGAAATCCG CATGCACTAA	600
AAAGTGTGTC TGCCTAAAAG TGTGTACAGC AGGCACAACC TTCCTTGTGG ATTTCCGTCT	660
GCTCACTGCA GATCTGCCTG TGGTTTAGAA ATAGAATTCA AGAGCCATCA AGGAGTGAC	720
AGCTTGACAC CACTGCCAAA TTCAGAATGA GGAACCTTGA GAGAAGGAAC TGTCGCTCAG	780
CCAGAAGCAG ATGAAGCCAC TGGTCCTGGT TCACAGTTA GTGTCATGCT CTGGTTATA	840

GAGCTCCTAT CCTGATTCTG AGATTTGAAA TAAAGCATGA ATGAACAAAG AAAAAA 955

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - ii) MOLECULE TYPE: cDNA
 - iii) HYPOTHETICAL: NO
 - iv) IMMEDIATE SOURCE:
 - (B) CLONE: HW018
 - ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 86..1102
 - (D) OTHER INFORMATION: /product= "predicted polypeptide"
 - ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: complement (644..994)
 - (D) OTHER INFORMATION: /label= SAC_23880

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTT TAT AAG ATC CCG ATC CTG GTC GTT AAC AAA GTC TTG CCA ATG GTC Phe Tyr Lys Ile Pro Ile Leu Val Val Asn Lys Val Leu Pro Met Val 110 115 120	448
TCC ATT ACC CTC TTG GCA TTG GTT TAT CTG CCA GGA GAG ATA GCG GCA Ser Ile Thr Leu Leu Ala Leu Val Tyr Leu Pro Gly Glu Ile Ala Ala 125 130 135	496
GTT GTG CAG CTT CGC AAT GGG ACC AAG TAC AAG AAG TTC CCA CCC TGG Val Val Gln Leu Arg Asn Gly Thr Lys Tyr Lys Lys Phe Pro Pro Trp 140 145 150	544
TTA GAC AGA TGG ATG CTG GCG AGG AAA CAA TTT GGG CTC CTC AGC TTC Leu Asp Arg Trp Met Leu Ala Arg Lys Gln Phe Gly Leu Leu Ser Phe 155 160 165	592
TTC TTT GCA GTT CTG CAC GCC ATT TAC AGT CTC TCG TAC CCA ATG AGA Phe Phe Ala Val Leu His Ala Ile Tyr Ser Leu Ser Tyr Pro Met Arg 170 175 180 185	640
CGG TCC TAC AGA TAC AAG CTG CTC AAC TGG GCT TAC AAA CAG GTT CAA Arg Ser Tyr Arg Tyr Lys Leu Leu Asn Trp Ala Tyr Lys Gln Val Gln 190 195 200	688
CAA AGC AAA GAA GAT GCC TGG GTT GAG CAT GAT GTC TGG AGA ATG GAG Gln Ser Lys Glu Asp Ala Trp Val Glu His Asp Val Trp Arg Met Glu 205 210 215	736
ATT TAT GTG TCC CTG GGG ATT GTG GGA CTG GCC ATC TTG GCT CTC TTG Ile Tyr Val Ser Leu Gly Ile Val Gly Leu Ala Ile Leu Ala Leu Leu 220 225 230	784
GCT GTG ACA TCT ATC CCA TCT GTG AGC GAC TCT TTA ACC TGG AGA GAA Ala Val Thr Ser Ile Pro Ser Val Ser Asp Ser Leu Thr Trp Arg Glu 235 240 245	832
TTT CAC TAT ATT CAG AGC AAA CTG GGA ATT GTC TCT CTT CTT CTG GGC Phe His Tyr Ile Gln Ser Lys Leu Gly Ile Val Ser Leu Leu Leu Gly 250 255 260 265	880
ACG GTA CAC GCT TCG ATT TTT GCC TGG AAT AAA TGG GTA GAT ATC AGT Thr Val His Ala Ser Ile Phe Ala Trp Asn Lys Trp Val Asp Ile Ser 270 275 280	928
CAG TTT GTC TGG TAC ATG CCT CCG ACT TTC ATG ATA GCT GTT TTC CTT Gln Phe Val Trp Tyr Met Pro Pro Thr Phe Met Ile Ala Val Phe Leu 285 290 295	976
CCA ACT GTT GTT CTG ATC TGT AAA ATT GTA CTT TGC CTG CCC TGC CTG Pro Thr Val Val Leu Ile Cys Lys Ile Val Leu Cys Leu Pro Cys Leu 300 305 310	1024
AGG AAG AAG ATA CTG AAG ATT AGA TGT GGT TGG GAA GAT GTC CGC AAA Arg Lys Lys Ile Leu Lys Ile Arg Cys Gly Trp Glu Asp Val Arg Lys 315 320 325	1072
GTT AAC AGG ACT GAG ATG GCC TGC AGG TTG TAGAACTACT GTTTGCACAT Val Asn Arg Thr Glu Met Ala Cys Arg Leu 330 335	1122
AATTGCTTAA TACCGATGTC TTATAAACAT TTCAACCTG TGTCTGTTAA TAAAATGAAT	1182

ACTTCTGGAT CAAAAA

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Glu Ile Ser Lys Asn Ile Thr Asn Pro Glu Glu Leu Trp Lys Met
 1 5 10 15

Lys Pro Lys Gly Asn Leu Glu Asp Asp Ser Tyr Ser Thr Lys Asp Thr
 20 25 30

Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Ser Pro Leu Pro His
 35 40 45

Thr Val His Val Asp Ala Phe Asp Cys Pro Thr Glu Leu Gln His Thr
 50 55 60

Gln Glu Leu Phe Pro Asn Trp Gln Leu Pro Ile Lys Val Ala Ala Val
 65 70 75 80

Leu Ser Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Ile Ile Tyr
 85 90 95

Pro Leu Val Ala Ser Arg Glu Gln Tyr Phe Tyr Lys Ile Pro Ile Leu
 100 105 110

Val Val Asn Lys Val Leu Pro Met Val Ser Ile Thr Leu Leu Ala Leu
 115 120 125

Val Tyr Leu Pro Gly Glu Ile Ala Ala Val Val Gln Leu Arg Asn Gly
 130 135 140

Thr Lys Tyr Lys Lys Phe Pro Pro Trp Leu Asp Arg Trp Met Leu Ala
 145 150 155 160

Arg Lys Gln Phe Gly Leu Leu Ser Phe Phe Phe Ala Val Leu His Ala
 165 170 175

Ile Tyr Ser Leu Ser Tyr Pro Met Arg Arg Ser Tyr Arg Tyr Lys Leu
 180 185 190

Leu Asn Trp Ala Tyr Lys Gln Val Gln Gln Ser Lys Glu Asp Ala Trp
 195 200 205

Val Glu His Asp Val Trp Arg Met Glu Ile Tyr Val Ser Leu Gly Ile
 210 215 220

Val Gly Leu Ala Ile Leu Ala Leu Leu Ala Val Thr Ser Ile Pro Ser
 225 230 235 240

Val Ser Asp Ser Leu Thr Trp Arg Glu Phe His Tyr Ile Gln Ser Lys
 245 250 255

Leu Gly Ile Val Ser Leu Leu Leu Gly Thr Val His Ala Ser Ile Phe

260	265	270	
Ala Trp Asn Lys Trp Val Asp Ile Ser Gln Phe Val Trp Tyr Met Pro			
275	280	285	
Pro Thr Phe Met Ile Ala Val Phe Leu Pro Thr Val Val Leu Ile Cys			
290	295	300	
Lys Ile Val Leu Cys Leu Pro Cys Leu Arg Lys Lys Ile Leu Lys Ile			
305	310	315	320
Arg Cys Gly Trp Glu Asp Val Arg Lys Val Asn Arg Thr Glu Met Ala			
325	330	335	
Cys Arg Leu			

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1801 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: HW032

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: complement (1412..1793)
(D) OTHER INFORMATION: /label= SAC_24831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTTTTCCAGC TTTTTAACGTT GCATTTATTT TTGATAATCT GTACTGTAGC CAATCAATT	60
TATTCTCCAT TCTTGCTTAA TTGTATTAGC CATAAAGGAG TTCAGGTTCA TAGGACTCAG	120
TTTCTCTATT AAACCGTCAT TGATTATGGA AATACTGTCT TAAGCACTAT GCAGATTAAC	180
ACCATACTT TCTTCCATTA CATCTTCAA GACAGTCACT CACAACTCAG AAGACTGATA	240
CAGCATTAGA TGAAAAAAAC AAGATTACAA GATATATGTA GTGAAACTCA AACTAGGAGT	300
CTTAGAGATA AAAAAGATAA GTAGATATTT AAAATGTAGT CTGTTAAAGA TTTAATCGGT	360
TTAAAGTATA AGATTAGAAA GACAAAGTTT CTATTGTTT GAAAGTTTTA AGTAAAGAAA	420
AAAAAACTGG AAAATATGTC TTTGTTGTTC TTTCTCCGTT CTTAATTACG AGCTATCCAA	480
CAGAAACCCC TAGGTCAAG TTTATGTTTC TGTTCTCATC AATGTAACCA GAACACTGG	540
GAAAGAAAAA GGAAGACATA TTAACCAATG GCCGCAATCA CTTTTCACTT GCCCCACGGT	600
ACAAATCTGA TTTGGATGAA ATGGTTTGTG GCATAAAAAT TTTAAATTTT AGAAGCCAAT	660

GTGGTAGATT TCTCCATGTT TGCACAAATC CAATTCAAC TACTTTACT TCACTAATTA	720
ATTAATGGA TTGGAAACAT TCTAGAAATG AAATTGTGTC TTTAGATGGA GTTGGGGAGA	780
GTACGCTTTA TTTAAATAT TTAGTCAAA TTTCATTTTC ACTTCTTGGT CTTATTATTT	840
CAGCTTCAGT TGGGGCTGGC TTCTGTGGG CTTACATGCT GACTGTGTCA GGCAGCTGGA	900
GGTGATCTAC ATTGACAGGA TTCAATGACT TTCTCCTCCG CGAAAAGCCC CTGTCAGCTA	960
CACAAGGATG GGAGGTTTTC GGACACTGT CAAGTGATTG CAGATCCTGA CTTCTCAAAT	1020
ATGAGGTGTC GGCAGTGGCA GCAGCAGCTA CTGGTAGCTG CCCCAGACTC CTCAGATAAC	1080
TTACACAGGA GCTGGTTTAT GCATCCCCCTT CGTCAGAGCT TCCTCTGGGC AAGTGAAAGT	1140
TGCAAGCCTT CACTTGCCTT CATGTCTCAG CTCTCTAAGT GACCCTGCCT GTGCTGGCCC	1200
TTGTGCTTAT GGTGGTGGTG GTGGTGGTGC AAGCCTGAAG GAGGAAGACT TGTCTCAAACA	1260
TCTAATGCCCTT CTGGTTGCTG ATTCTCTGAA GGCTTACTGC TCCCAGCAAC CGTCAGCCTC	1320
AGTCGCAGCC GGGCCTCGCT CCTCAACTTG GCAAAAATGC CTACAGAGAC TGAGAGATGC	1380
ATCGAGTCCC TGATTGCTGT TTTCCAGAAG TACAGTGGGA AGGATGGAAA TAGCTGTCAT	1440
CTCTCCAAAAA CTGAGTTCCCTT TTCCCTCATG AACACGGAGC TGGCCGCCTT CACGAAGAAC	1500
CAGAAGGACC CCGGTGTCCT CGACCGCATG ATGAAGAAC TGGACCTCAA CAGTGATGGG	1560
CAGCTAGATT TCCAAGAGTT TCTCAACCTT ATTGGTGGCT TAGCTATAGC ATGCCATGAG	1620
TCCTTCCTCC AGACTTCCCA GAAGCGTATC TAACCCCTCTC CATTCCCTTC CAGCCACCAA	1680
GTCATGCCT CCTCCACTCC TTCCCCCATC CACACCTGCA CTGAGCCCAC CACACCTACC	1740
ACACATGCAG CCCACGCCCTG ACAGGGAAAAA TAAAACAATG TCATTTTTTT AAATGTAAAAA	1800
A	1801

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2646 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HW033

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 50..263
- (D) OTHER INFORMATION: /label= SAC_23901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTCGACTTGA CTTCTTAGTT TTCTGACGGG AGCTCTCTTC CTTCTGAGTA CTAGTCTCGG	60
GCCTCCAGCC CCAGGAAGAC CCTCTGCTTT TCTCTCCACC CTTGGCTTGC TCCTCAGCAG	120
GGAAGAAGTA GATCACAGTC TCACTGCCCT CAGTCCCAG CTTTGCCAGT CACCAGCTGT	180
GTAGTCTCAG GCCAATCACC ACCTCCTCTA GCCTAGGTAG TTGGTTTTAT GTGGGTGAAT	240
GTTTTGCCTG GATGTATGTA TGTACACCAC CTGTGTGCCT GGTGCCCTG CAGTCAGAAG	300
AAAGTCCAC ACCCCTAGGA ACTGGAGTTA AGATGGGTTA GAGCCTCCAT GTGGGTGCTG	360
AGAACTGAAC CTGGTTCTCT GGAAAAGCAG CCGGCACCTCA ACCTCTGAGC CAGCTCTCA	420
TCCCCGAGTC CGTTTATTAA ACCGGCTATA AAATGGATTT AAAACGACTT ACCTCACCAG	480
GCCTGTGAAA CATTAAAAAA CTTAATAAAA ATTCTACACT TAATTGTTTT TGCTTATGCT	540
TTCTAGTCCC TTTAGTCTTA GACAGTTCT GTTTCTTGTAA TTTATAAAAGT TGGTATTAAA	600
TATATAGCCA GTGGACAAGA ACCTTACTGC TATGGGCTGG CCCCTGTAGG GTCCTAGACT	660
AGAGGAGCGT ACTTTGTGGT TTAAAGTGGT TTGGCCTGCC TACCTGTTTT TCCCACGTGG	720
CTCAAAACAC TAATAAAGCA GGGGTGACCT GTGTCACCTG AGCATTGAGC AGAACACTGG	780
CCCAGGCAAT GGCTCAAAG CTGGGCTACA TTATAAAAGT AACCTTCTTG TTCATACTGG	840
GTCACAGAAG CAGGCCAGA AAAAATAAAA AATCCTGGTC ACTCGGTTCC CCCCTGCACC	900
ATCATCTGTT CACTAGTGC CCTCTGACCA TTCTCACCCA AGACAGGCAT CCTCTGGAA	960
CCTTAGGCAG GTCCATTCTC TCTTGTCAAT TTGGAATGAA GCACTAACAG CCCTGGGTC	1020
TCTGCCATTG GCTTCCCAGA GTGTCCAAT GAGTTTCGT GAAGGAATCT GGGTTTATCT	1080
TTCCCGGGCT TCCTGCCCTG TTAGCAGAAT TTCAAAATAGC AGATAATAGA TTCTGACCTG	1140
TGAGGCCATT TTTCTCTCAA TCCCTTCTT CTGAGACATT AGCCTGGGC ATGCAGCAGC	1200
TGCGCACTGG TTTCAGGGAG GAAAGGGGTG AATGGTGAGC GAACTGGCC CTGTGGATGC	1260
TAACCTCACT GAGATGAAAA CATGGGGCT TTTCTCTGAA GACGCAGGGC CGTGTAAACA	1320
TATGACTTTG ACCATATTCT CAGGTTGGG GATGTGGAA GTTCCAGGAA CAGAAATCCC	1380
CTGCTGAGTT CTTGGCACT GTGGCTATTT GTTCCCATGA GGACCTCTCC CTGCAGTCTG	1440
CCCTCTGGCA GGGTGGAGTA TAGAAGACTC AAGAGCTACA GATGCCCGCG TCACTGGAGC	1500
TCCCCCTGCAC CTAGGCCATC AATCACGTCC ACCATCACCA GAGGGCTTA GGCCTAGGGT	1560
GTATGCTGAG GGAAAGACGA GGGCCTGTCC CACTACTCGA GTAGAGCAGA TGGCCTTCTG	1620
TGTAGGCAGT GAATTTCATA GCAGTGCCTT GAGGAGCCCA GCATGTTCTC AAGCACCTCC	1680
TCCCAAGTTA TATTTGGAAG TCTGCTTCAC AGGGACCAGA GGGCATAAAC CTAACCTACC	1740
CACTTCCCAT CAGGGACAGC CCAAAGCACA CCAGTATATG TAAGGGGTGC AGGGAGGTAT	1800
CATGGGTCTC TTCTCTCCTC TCAGTGCTCA AACTCAGGTG GAGGCTATGG ATTCAAGGATC	1860

TTGGTTAGGA GTTGCAAGCA ATGGACAAGA AAGAGCATTA GGGAAACCAG AATCCCAGCC	1920
TGTCCCTGTG CCTCCACCCC AGCTAGACTT GAGGCTTAGG TCCTGATACT CTGCCCTTAC	1980
ACACCCCTCTC TCCATTCCCC AGGAGTTAGT AAAAAACAGG CAAGGGTAAT ATGCTATCAT	2040
CTGTGGTCCT GAGCCTTCTC CAGACTCCCC CTTCACTCCG CGGCCACTGC CACCACCA	2100
GAGACATCTT CGGAAGCATT AGGTTTATTT CTTGAAGTGA ACTCCTGGGG AGAAGATGAC	2160
TGGTGCCACC ACATGTGCTC TGCTGGTTA GGGGCCTTGA GGTGGCACAG TCCAGCCATA	2220
GAAGGATCAG CCTTCCTGCC CATAAGATT AATGCCAGGG AGTCAGATAG TTGATGCCAC	2280
TGTAAAGAGA AAGAGAGGTG AGATGGGAC TCCAAGGTAC TGTAAGAGA AATCAAGTTT	2340
TTCTTCCTTA GCTCCATCCT CCACCTCCAAA GCCTCAGGGA TCTGAAAACA GTCTTCATCC	2400
AGTCTATGTG CCCACAACCT TCAATGGTTC CCTACTTCCT CTTGTATATT TTTGGCTATT	2460
CTCTTCACCT CTAATTAGCT CATACTGTTT CCCACTGACT CCCGTCTTTA ATGGCTTCAT	2520
AGGTTTTCAAG TCACGTATGA ATCTACACTG CATCACACAG TTACAAAACC CAGAGTTGGG	2580
GTTGGGGATT TAGCTCAGTG GCCTAGCAAG CGTAAGGCC CGGGTTCGGT CCCCCAGCCCC	2640
AAAAAA	2646

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HW034

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 91..837

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 3101..4162

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 3561..3862
 (D) OTHER INFORMATION: /label= SAC_23897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTCGACGGAA GAGCTGTTGT GACTGCGGTA CTGCGGAGGG CTCTCGGCGG CCCGCGACAA	60
GGCTGAGTCC CGGGAGGTCC ATGCCCCACC ATG CTT TCC TGT GAC ATC TGT GGT	114

	Met	Leu	Ser	Cys	Asp	Ile	Cys	Gly
1						5		
GAA ACT GTA ACC TCA GAA CCA GAT AGG AAG GCT CAC CTA ATT GTT CAC								
Glu Thr Val Thr Ser Glu Pro Asp Arg Lys Ala His Leu Ile Val His								
10	15					20		
ATG GAA AAT GAA ATT ATC TGT CCG TTT TGC AAG CTG TCG GGT ATA AAT								
Met Glu Asn Glu Ile Ile Cys Pro Phe Cys Lys Leu Ser Gly Ile Asn								
25	30			35		40		
TAC AAT GAA ATG TGT TTT CAT ATT GAA ACC GCT CAT TTT GAA CAG ACT								
Tyr Asn Glu Met Cys Phe His Ile Glu Thr Ala His Phe Glu Gln Thr								
45		50				55		
ACG CCA GAA AAA AGC TTC GAG ACG CTA GCC GCA GTG CAA TAT GAA AAT								
Thr Pro Glu Lys Ser Phe Glu Thr Leu Ala Ala Val Gln Tyr Glu Asn								
60		65				70		
TCA GAC CTC GGT AAT ACC AAG CTG CAC AGT ACA GTG GAA GTT ACC TCA								
Ser Asp Leu Gly Asn Thr Lys Leu His Ser Thr Val Glu Val Thr Ser								
75	80			85				
GGC ATC CAT TCA GCT TGT GCA TCG AAC TTT CCA AAG GAG TCG TCC GAA								
Gly Ile His Ser Ala Cys Ala Ser Asn Phe Pro Lys Glu Ser Ser Glu								
90	95			100				
AGC CTT TCT AAA GAT AGG ACT TTA AAA CAA GAA GCT TTT TAT ACA GAG								
Ser Leu Ser Lys Asp Arg Thr Leu Lys Gln Glu Ala Phe Tyr Thr Glu								
105	110			115		120		
AGC GTA GCT GAA TCT AGA AAG TAC CAG AAA AGC AGA GAA AAG CAG TCC								
Ser Val Ala Glu Ser Arg Lys Tyr Gln Lys Ser Arg Glu Lys Gln Ser								
125		130				135		
GGA TTG TCT GAG GCC CAA GGA TCA ATT TAT GAA ACA ACA TAC AGT CCC								
Gly Leu Ser Glu Ala Gln Gly Ser Ile Tyr Glu Thr Thr Tyr Ser Pro								
140		145				150		
CCC GAA TGT CCG TTC TGT GGG AGA ATT GAG AGG TAC AGT CAA GAT ATG								
Pro Glu Cys Pro Phe Cys Gly Arg Ile Glu Arg Tyr Ser Gln Asp Met								
155		160				165		
GAA ATT CAT GTG AAA ACA AAG CAT GCC AGC CTT CTA GAA AGT CCG TTA								
Glu Ile His Val Lys Thr Lys His Ala Ser Leu Leu Glu Ser Pro Leu								
170		175				180		
GAA GAC TGT CAT CAA CCA CTC TAT GAC TGT CCC ATG TGT GGG CTT GTC								
Glu Asp Cys His Gln Pro Leu Tyr Asp Cys Pro Met Cys Gly Leu Val								
185		190			195		200	
TGT ACA AAT TAT CAC ATT CTC CAA GAA CAT GTG GAC TTG CAT TTA GAA								
Cys Thr Asn Tyr His Ile Leu Gln Glu His Val Asp Leu His Leu Glu								
205		210				215		
GAA AGC AGC TTT CAA CAA GTA CTT GTG AGT GGG TAT GTG CCT GTG TGG								
Glu Ser Ser Phe Gln Gln Val Leu Val Ser Gly Tyr Val Pro Val Trp								
220		225				230		
ACA CCC GAC CTG CGA TGT CAT CCT CAG GAA GGC CGT ACA ACT CCT TTA								
Thr Pro Asp Leu Arg Cys His Pro Gln Glu Gly Arg Thr Thr Pro Leu								
235		240				245		

AGA TGAGTTCTT AGTATCTGG AACACACCAG TTAAGCTCCC AAGTTTGCTT Arg	887
CTATCTCCAC CTCCCTAATA ATGCTGGAGT TACAATCATG GACAACCATA CACACATGTT	947
TCACATGATT CTGGGCAGTG AGCTTAGGTC CTTATGTCTG TGAGGCAAGC TCTTCCTGAC	1007
CGAGCTATCT CCTGAGCCTG CTGTCTGTCT CTTTAAATAA TATTAATAAC TTCATATAGA	1067
GCTCTCGAAG GTATAGGGTC TTGTATGAGT CTCCTAGGGC CACTGAAAAA TAAAGTGACC	1127
TCTAAGAGAA GTTGTGTATA TTTTTATTAC TCTGTCAGTA TTTGGGAGTA TGTAGACAGC	1187
TCCTGGTAAA GTAGGAGATT TTAGCGITCG ATGATTTACC ACCAATAACC GTGATCTCTA	1247
TGCATCATGT ACCTGCTTTG CTCATTACCA CAAGAGGAAA ATTAGTAGAA TATTCTTTT	1307
TTTCCTTTTC CTTTTTTTTTC TTTTTTTCGG AGCTGGGGAC CGAACCAAGG GCCTTGCACT	1367
CGCTAGGCAA GCGCTCTACC ACTGAGCTAA ATCCCCAACC CCAAATTAGT AGAATATTGA	1427
TGGAAGATTA TTTCACGTCA GTGGTCTTCT GCTGTCTACC CCAGTTGGCA TGCCACTGTC	1487
GTTGTTTAGG GTTCCCTGTTG CTGTAATAA ACACTACCAA CAAGAGTAAC CTGGGCAGGA	1547
AAGGGTTAT TTTATCCAAA CATTCCAGT TCACCACTGA GGGAAATTCAG GGAAGGGACT	1607
CAAGGCAGGA ACCTGTAGGC AGGAGCTGAT GCAAAGGCCA TGAAGTGCTG CTGAGTGGCT	1667
TGTTTTGCCCG TGACTTGTTC AGACTCCTTT CTTAGAGCAC CCAGGGATAT CAGCCCAGGG	1727
GTGGCATCAC CTACAAGGAC TGGGCCTTCC AACACCCAGTC ACTACAGAAC GCACTACAGA	1787
CTTGCCTGCA CTCGGTCTTT CTTTACTGTT GTATTGTTTT TTGAGATGGA GTCTCACTAT	1847
GTAGCTCTGG CTAAGTGTAA ACTCTAGCTT GTGTCAAGTT GACCTAAAAC TAGCCAGCAC	1907
AGCTATCTTC CTTTGAGTAA GATTGTAAGA GGATGCTGTG GAAGGGTAA TTTTTTCAA	1967
GCAGAACATGTC TGATAATTCT TACTTTAGGG ATAGGCTTTG TATTGTATTC TATAAACCAA	2027
TGAAACAGTC TCAGGGCATG CTAAAATCA GTTGTGCAGT ACATGCCAA GAGTGGAAC	2087
TAGAACAGT GGGAAAGGTGT AAAATGGGTT AATCAACAGG TGTGTGCATT GTACTGTCTC	2147
TGAATTGAGG AGTACCTAGA AGACTCCTAA CTGTTCTTC TGGGTGTATC TCTGAGGATG	2207
TTTCAGAAT AACTGATGGG TGCCTGGCA AACAGAACGA AGAAGATGTG CATTCAAGCGT	2267
GGGCAAGTAG TGTCCAGTGT CGCTAGTACT ATAGGTGGAC CAGGAAAGCC GAAGCAGTGG	2327
CAGAACACT TTGGCTCCTC CTTCTGGATG GGGCTTCCTT TCCCTGCAGC TGCTCCCTGG	2387
GTGCAGCTGC TCCCTGGGTT ATACTCCAGG ATGTCTGACT TTTGGATGCT GGAACCTCTGA	2447
TAATCCCTAC CAGAAATTAA GAGCCTTGA CCTCACACTG GGATATCTGA TTTTGCCAAA	2507
CTGGTTCTGG CACTTTCAAC TTTCACTACT GGTTCTCTG TGTCTCAGGC TATCAAGAAC	2567
TTTTCAATTG TATCATTATG TGATCTATTC CGGTATGATT CGTGATATTT AATAAGGTTT	2627
TCTATATCTT TCTGTCGTGTC TGTCTCTGTG TGTGTGTGTA CATAACACACA CACGCCTGTG	2687

TGTGGTGTTC TCTTATCTTG CCCTCAGTCC TGTTACTGGA GGACCCTGAC CAGTAAAGAA	2747
TTTAGGAAAC AAGACTCAAT ACATTACAAT ACAATACAAG CCATTGACTA AAGAATCTGA	2807
GTTTCAGTGG GAGAGAGGAA GCATGGCATT ATGCTATAAA ATTATTTCAGC TTGTTCGGGT	2867
AAAAACTGTA ATGTAATGAA ACAGTTGGAG GTTGTGAATA TATATTTTAT ATTATTTATT	2927
AGTTTTTTCT TTCCATTAGT TGTGTTCAGA GATATCAATG ATAAGGGTCT TTCAACCGCT	2987
CA C CTTTGT TTTTCTCCCT AAAGGTGTTA GGATGTCAC AATTGCTAGT TAATGAGAAA	3047
TGCTTGTTAG AGCCTAACCA CTGACTCATT CGGGTTGTCC CTCTCCAATA GGC ATG Met 1	3103
GAC AGA GTC CAG TGT TCT AGT GAC AGA GAA TTA GCT CAC CAG CTT CAG Asp Arg Val Gln Cys Ser Ser Asp Arg Glu Leu Ala His Gln Leu Gln 5 10 15	3151
CAA GAA GAA GAG AGA AAG AGG AAA TCT GAA GAA TCA AGA CAA GAA AGG Gln Glu Glu Glu Arg Lys Arg Lys Ser Glu Glu Ser Arg Gln Glu Arg 20 25 30	3199
GAA GAG TTT CAG AAA TTG CAG CGG CAG TAC GGC TTA GAT AAT TCT GGA Glu Glu Phe Gln Lys Leu Gln Arg Gln Tyr Gly Leu Asp Asn Ser Gly 35 40 45	3247
GGA TAC AAA CAA CAG CAG CTG CGA CAC ATG GAG CTA GAA GTA ACG AGG Gly Tyr Lys Gln Gln Leu Arg His Met Glu Leu Glu Val Thr Arg 50 55 60 65	3295
GGA CGA ATG CAT CCA TCT GAG TTC CAC AGC AGA AAA GCT GAC ATG TTG Gly Arg Met His Pro Ser Glu Phe His Ser Arg Lys Ala Asp Met Leu 70 75 80	3343
GAA TCA ATC GCT GTT GGT ATT GAT GAT GGA AAA ACA AAA ACT TCT GGA Glu Ser Ile Ala Val Gly Ile Asp Asp Gly Lys Thr Lys Thr Ser Gly 85 90 95	3391
ATT ATT GAA GCC CTC CAC AGG TAT TAT CAG AAC ATT GCC ACA GAT GTA Ile Ile Glu Ala Leu His Arg Tyr Tyr Gln Asn Ile Ala Thr Asp Val 100 105 110	3439
AGG TGT GTG TGG CTG TCT ACA GTG GTG GAT CAC TTT CAT TCA TCT TTT Arg Cys Val Trp Leu Ser Thr Val Val Asp His Phe His Ser Ser Phe 115 120 125	3487
GGG GAC AAA GGT TGG GGT TGC GGT TAT AGA AAT TTC CAG ATG CTG CTT Gly Asp Lys Gly Trp Gly Cys Gly Tyr Arg Asn Phe Gln Met Leu Leu 130 135 140 145	3535
TCA TCA TTA CTG CAG AAT GAA GTG TAC AGT GAC TGC TTG AAA GGT ATG Ser Ser Leu Leu Gln Asn Glu Val Tyr Ser Asp Cys Leu Lys Gly Met 150 155 160	3583
TCA GTT CCT TGT ATT CCA AAA ATT CAG TCC ATG ATT GAA GAT GCG TGG Ser Val Pro Cys Ile Pro Lys Ile Gln Ser Met Ile Glu Asp Ala Trp 165 170 175	3631
AAT GAA GGT TTT GAT CCT CAG GGG GCC TCT CAA CTT AAT AAC AAG TTG Asn Glu Gly Phe Asp Pro Gln Gly Ala Ser Gln Leu Asn Asn Lys Leu	3679

180	185	190	
CAG GGG ACC AAG GCC TGG ATT GGA GCA TGT GAG ATC TAT ACA CTT CTG Gln Gly Thr Lys Ala Trp Ile Gly Ala Cys Glu Ile Tyr Thr Leu Leu 195 200 205			3727
ACC TCA CTG AAA GTC AAG TGC CGC ATT ATT GAT TTT CAC AAG TCA ACT Thr Ser Leu Lys Val Lys Cys Arg Ile Ile Asp Phe His Ser Thr 210 215 220 225			3775
GGT CCT TCA GGC ACA CAC CCT CGC TTA TTC GAG TGG ATA CTG AAC TAT Gly Pro Ser Gly Thr His Pro Arg Leu Phe Glu Trp Ile Leu Asn Tyr 230 235 240			3823
TAT TCC TCA GAG ACG GAA GGG GCG CCA AAG GTC GTG TGT ACA TCC AAA Tyr Ser Ser Glu Thr Glu Gly Ala Pro Lys Val Val Cys Thr Ser Lys 245 250 255			3871
CCT CCT GTC TAT CTC CAG CAT CAG GGT CAC AGT CGA ACA GTT GTT GGG Pro Pro Val Tyr Leu Gln His Gln Gly His Ser Arg Thr Val Val Gly 260 265 270			3919
ATT GAA GAG AGA AAA AAC CGA ACA TTA TGT TTG CTA ATA TTT GAT CCT Ile Glu Glu Arg Lys Asn Arg Thr Leu Cys Leu Ile Phe Asp Pro 275 280 285			3967
GGA TGT CCT TCT CGA GAA ATG CAG AAG CTG TTA AAG CAA GAC ATG GAG Gly Cys Pro Ser Arg Glu Met Gln Lys Leu Leu Lys Gln Asp Met Glu 290 295 300 305			4015
GCT GGT AGT CTC AGG CAG CTC CGG AAA TGT GTG GGA AAT CTG AAG CAT Ala Gly Ser Leu Arg Gln Leu Arg Lys Cys Val Gly Asn Leu Lys His 310 315 320			4063
AAG CAG TAC CAG ATA GTA GCA GTG GAG GGT ATC CTG TCC CCA GAG GAG Lys Gln Tyr Gln Ile Val Ala Val Glu Gly Ile Leu Ser Pro Glu Glu 325 330 335			4111
AGA GCT GCC AGG AAA CAA GCT TCT CAA GTG TTT ACA GCG GAG AAG ATT Arg Ala Ala Arg Lys Gln Ala Ser Gln Val Phe Thr Ala Glu Lys Ile 340 345 350			4159
CCT TGACCCAGAT ATTTTGTAAAT TATCCTTTTT GTTTCCGATA TTGAACCTCTG Pro			4212
ATACAGTTGA AGAATTTGAC TTCACTGAAG TCGGTGATAA ATTATTTAAG TTATAAATGC			4272
CTGTTGTACT CCTTAGCATT TCGTTGTCTG GTAATCAGTT GAATAAAATTC CTTGTTTACA			4332
TTAAAAAA			4339

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Leu Ser Cys Asp Ile Cys Gly Glu Thr Val Thr Ser Glu Pro Asp
 1 5 10 15

Arg Lys Ala His Leu Ile Val His Met Glu Asn Glu Ile Ile Cys Pro
 20 25 30

Phe Cys Lys Leu Ser Gly Ile Asn Tyr Asn Glu Met Cys Phe His Ile
 35 40 45

Glu Thr Ala His Phe Glu Gln Thr Thr Pro Glu Lys Ser Phe Glu Thr
 50 55 60

Leu Ala Ala Val Gln Tyr Glu Asn Ser Asp Leu Gly Asn Thr Lys Leu
 65 70 75 80

His Ser Thr Val Glu Val Thr Ser Gly Ile His Ser Ala Cys Ala Ser
 85 90 95

Asn Phe Pro Lys Glu Ser Ser Glu Ser Leu Ser Lys Asp Arg Thr Leu
 100 105 110

Lys Gln Glu Ala Phe Tyr Thr Glu Ser Val Ala Glu Ser Arg Lys Tyr
 115 120 125

Gln Lys Ser Arg Glu Lys Gln Ser Gly Leu Ser Glu Ala Gln Gly Ser
 130 135 140

Ile Tyr Glu Thr Thr Tyr Ser Pro Pro Glu Cys Pro Phe Cys Gly Arg
 145 150 155 160

Ile Glu Arg Tyr Ser Gln Asp Met Glu Ile His Val Lys Thr Lys His
 165 170 175

Ala Ser Leu Leu Glu Ser Pro Leu Glu Asp Cys His Gln Pro Leu Tyr
 180 185 190

Asp Cys Pro Met Cys Gly Leu Val Cys Thr Asn Tyr His Ile Leu Gln
 195 200 205

Glu His Val Asp Leu His Leu Glu Glu Ser Ser Phe Gln Gln Val Leu
 210 215 220

Val Ser Gly Tyr Val Pro Val Trp Thr Pro Asp Leu Arg Cys His Pro
 225 230 235 240

Gln Glu Gly Arg Thr Thr Pro Leu Arg
 245

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Asp Arg Val Gln Cys Ser Ser Asp Arg Glu Leu Ala His Gln Leu
 1 5 10 15

WO 98/53071

Gln Gln Glu Glu Glu Arg Lys Ser Glu Glu Ser Arg Gln Glu
 20 25 30
 Arg Glu Glu Phe Gln Lys Leu Gln Arg Gln Tyr Gly Leu Asp Asn Ser
 35 40 45
 Gly Gly Tyr Lys Gln Gln Gln Leu Arg His Met Glu Leu Glu Val Thr
 50 55 60
 Arg Gly Arg Met His Pro Ser Glu Phe His Ser Arg Lys Ala Asp Met
 65 70 75 80
 Leu Glu Ser Ile Ala Val Gly Ile Asp Asp Gly Lys Thr Lys Thr Ser
 85 90 95
 Gly Ile Ile Glu Ala Leu His Arg Tyr Tyr Gln Asn Ile Ala Thr Asp
 100 105 110
 Val Arg Cys Val Trp Leu Ser Thr Val Val Asp His Phe His Ser Ser
 115 120 125
 Phe Gly Asp Lys Gly Trp Gly Cys Gly Tyr Arg Asn Phe Gln Met Leu
 130 135 140
 Leu Ser Ser Leu Leu Gln Asn Glu Val Tyr Ser Asp Cys Leu Lys Gly
 145 150 155 160
 Met Ser Val Pro Cys Ile Pro Lys Ile Gln Ser Met Ile Glu Asp Ala
 165 170 175
 Trp Asn Glu Gly Phe Asp Pro Gln Gly Ala Ser Gln Leu Asn Asn Lys
 180 185 190
 Leu Gln Gly Thr Lys Ala Trp Ile Gly Ala Cys Glu Ile Tyr Thr Leu
 195 200 205
 Leu Thr Ser Leu Lys Val Lys Cys Arg Ile Ile Asp Phe His Lys Ser
 210 215 220
 Thr Gly Pro Ser Gly Thr His Pro Arg Leu Phe Glu Trp Ile Leu Asn
 225 230 235 240
 Tyr Tyr Ser Ser Glu Thr Glu Gly Ala Pro Lys Val Val Cys Thr Ser
 245 250 255
 Lys Pro Pro Val Tyr Leu Gln His Gln Gly His Ser Arg Thr Val Val
 260 265 270
 Gly Ile Glu Glu Arg Lys Asn Arg Thr Leu Cys Leu Ile Phe Asp
 275 280 285
 Pro Gly Cys Pro Ser Arg Glu Met Gln Lys Leu Leu Lys Gln Asp Met
 290 295 300
 Glu Ala Gly Ser Leu Arg Gln Leu Arg Lys Cys Val Gly Asn Leu Lys
 305 310 315 320
 His Lys Gln Tyr Gln Ile Val Ala Val Glu Gly Ile Leu Ser Pro Glu
 325 330 335
 Glu Arg Ala Ala Arg Lys Gln Ala Ser Gln Val Phe Thr Ala Glu Lys
 340 345 350

Ile Pro

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2415 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: HW035
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: complement (1738..1910)
 - (D) OTHER INFORMATION: /label= SAC_24468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GTCGACGGGC CCTATTCTGC CTCCCTCAGG ATCTGCGTCT TCCAGGGATC CGCTGTTCGA	60
CTTGGAGGTG CTTCTCTGCA GGTCCCAAGC CTGCCCTCCTC ACCCCAGCTT TCCAGTGGAG	120
GCTGCCCTCT TCCAGGCTTG GCTCAGGAAG CTCCTCATAG GCGGATGCC ACCCATAAGA	180
GGCTACATCC CTTTGTGGTC ACATGGCCTG TAGCCTCTTG CTGACATTGC TGGTGTCTTC	240
TCTGGGGCCC TGGATCCCTG ACAAGCACAG AAATGTGATC TGGTAAAAGG AAAGACTGTG	300
GCCTGATAGG CCTTTACCTC GTAGGCAGCA GGATTTCAC TCAGTTGAC ACAGCATGCA	360
GTGCTCTGGG AGCAGGACCT CTGCCACCTC GGCAATTTTG GTAGGCTGGT TTGGCTCAAG	420
GTGCTCAGAC ACTCCCATTG ATGCCTGAGT CGGATATGGG TGGAAATCTG GACTGTTGAT	480
TATAAGTTAC CAGGTGACCT CATTCCCTCC CTTTGTCTCT TAACTGGTAT CCAGTGAGTT	540
GCTGATGCCG ACTGGCAAGC AGAGCTGCC CATGCCCTAGA GGAGGAGAGG GACAGGCTTT	600
CTGAGTGCTT TGATTCTGGC TGGGCTGTAG TGTATAGCTG AGAATGGCCT CCTGCATGGG	660
TCCAGCCTTT TGGGAGGATG AGGAAGAGGA GGCTGAGGCT AGATGTGTGT TAAACAGGAG	720
TAGCAGATCT TTGCTCTGA ACCGGATAGA GCCGTGCTCA AGGTTTCAG GTTGCAGTA	780
TCTTCTTATT GAGTCTGGG AACGTTCCCT ATTGAGCCAG CCCTGCAGCT CCACTCCCTG	840
CCCCATTCCC CTGATTTCTT GACAGTAAAT CCTGTGTCCA GTTGTGACTG TTGGCTGTTT	900
TCCTGATCAT TGTAAATTCC GTTTTCCTAC TGTGAGGGTG TTGTGTTGA CTTTCTGACA	960
CAGCGAATGG AGAGCTTGGG CTGAGGCCAG GTCTCCAAA CTTCTCCGCT AAGTAAACCG	1020
TAATGTGTGA CTTCCCTCCT ATCTTGACTG CCCGACTCCT TCCTTCCACA TGGACACTCA	1080

GATTCAGAAG AAAACCCGCA GGAGGTGGGT CAGTTCCCTC TGTAGAATAT GGTCCCAGAG	1140
AGTCCTCCCC TCTGTTGTGT CTAGCTGCTA GTCTGGGTGT TGTACCATCA GTGCAGGGAG	1200
TCCACGGCAA CACTGAGTTA TACAGGGACC ACTACCATCG CCAGGCTTCC TAGCAGGCTG	1260
TTCTCAGTTC ATCTTCAGG TCCGTGTGTA CTCTGTGCTA GCAGCAGCCT TGGTGTCAA	1320
GGCCAGGATT TGCGAGTTTG ATAAGCTACA GCCCACTTGG AGATGGTGAG GCCACTTCCC	1380
TGCTACCTCC CTCTCTGGTG TGGCCACTTG GCCAAAGCTC CCATCCACAG CTGGGGTGTC	1440
TGAGCCACAG CCTGCTACAC TGTTCCGCT CTGGGATCTT CTGAGTTACT CTTTTAGGCT	1500
GTGGTTGGT GAAAGGAACC AACACATTAA CGATCTCCCC CCCCCCCCCC AAAGCCACTG	1560
AGTAATTCTT GGCATGTTTT CTAAGTGCTG TTGGCTGCCT GGTTTGGGAG CAGTTGTGGA	1620
GAGGACAGAC TTAGTACAC ACAGAGGCAT GGGTGTGCGA GCTGCTCACA GCTTCCTTGT	1680
TTCTGGCATG TGTCTGGGT GCGTGCTATA CCTCCCGGGC CAGCTGCACA CCTATGTACT	1740
CTGCCCTGA GAGGTAGAGT GTTCAGGAAG TGTCCCTGAT AGATTCCCTG TTCTCTGTGG	1800
CCCCAGTTGG GCTTTGGCT CCTCCAGCAA CTTCATGCC CAACCCTACC TTTCCCTCCA	1860
TTTCTCTCTG TCTGCTAGTC CCTGAAGCCT TTAACCAAAT GGGATGGGT ACAGAAAGCC	1920
TTCTCCTGGC AACTTAGGGC AACAGGACAA GGGCTATTGT GTGTCCAAT CTGTTGGTCT	1980
CCTGGTGCTG AGAGGTGTGT CCAAGCAGAG TTGATCAGCC CCTGCCTGCC CTGCAGGGCT	2040
GAAGCCAGGG GGAGGTTAGT AGAGAGTACC CTAATGGGG TGAGGGTCCT TAAACATCCA	2100
AGTGAGGAGG GGCTGTTGTG TGGCTGCAAG GTGAGACCT GTCTCCAGCA CCTGGGTAGG	2160
GCCATCGGGG ATCTGGCTGC AAGGTGAGGT CTGGACTTGG CATCAGTGCA GAGCGATCAA	2220
GTCACCTGGC CTCAGCAGGC AGCAGCCTTG GTGCCACCC GTGCCCTGCC CAGTATTAT	2280
TGCTAAATTA TTGTCCAGGA GGGGCGGCAC TGGGCCTGGC CCCCCGGGTA TTTATTGCTG	2340
TACATAGTGT ATGTTTGTGA TATATAAGGT TTTCTTTATT TTGTATATGA TCAATAAACG	2400
CCTTTAAAG AAAAA	2415

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3531 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HW036

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: complement (2541..2575)
- (D) OTHER INFORMATION: /label= SAC_24406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTCGACTGAA AACCACTCAG AATTTCTCT GGTCCCTAAC AGAAAAGAAT CAAAGTAGGA	60
AGCACAGTAG CTGCCACATC TGTTCAACCT CTGGGCCTCC CAAGTACACC AGAGAAAACA	120
GATCAATGCT GTTCTGAAT GATTCTGCTG GTTAAAGTCA TTTATAGAAG ATTACCGATA	180
CTGAACAACT ATGGGTTAAG AACTTACTGT GTTTTGTGAA TTGCCCAATG GAGAGAGTGT	240
GTTCAAGGAT GACTCTTGAT CAGATTACAC AGTATGTGCA TCCAGGAGGC CACATGAAAT	300
CAGCATAGTT AGTAACATAG AATCTGTTGT CAGCCTCCTC CAACTCGTGT CTGTTCTTG	360
GTTCAATTT TAGGCCAGCC CTCTCCTCAT AAAGGGGTGA TAGTAGCCAC AGTCCACAGC	420
CTCAAGGTCT GGTCTCCAAA AAGAAGAGTG TGAGCTGGGC CACAATCATA CCCTCCTGAA	480
GAACCTGGT CTTTCTGGT CATATGCTCC TGCCCCACCC TTGGTGATCC TGGCTAGATC	540
ATGGTCTCCC GTACTGTGCC GACACCATTG ACAGTAACAT AGGATGAGTT ATGGGCCTCA	600
TCCCTAAACA CTGGAACATTG CAGCAAATGA TGTAGCAGAT ATTCACTCTA GATAACAAAT	660
GTCAGTGACA TGAAGTGGCT AGGAAAAGTTT AGAACCTGAA TCATTTTATT TTTACCACTT	720
AACACAGTAG AGAGCCATCA GGACTAAATC TTTGGTGTGA TTCTTGCCAT TGAAGTCATT	780
ATAGCTTCCA TATTGTTCCG TAGTTCACTG GAAAGTGCAC TTGCTGTTAA AAGTTTGAA	840
GCTGTGAGGA TTCCCTAGGG TGTCACTGAA GTCTGCTCTG TATACTGCC CCACTGGGAG	900
TGCACGGTAC TGCACCCCTTA AATCCTGCCG CCTGTGTCCC AAACATGGTG TCTGCGTGCA	960
GTGTGGAGTA GTGCGCCTTC TTTTTTTTTT TTTTTTTTTT CCTATTCTTT TTTTGGAGCT	1020
GGGAACCGAA CCCAGGGCCT TGTGCTTGCT AGGCAAGTGC TCTACCACTG AGCCAAATCC	1080
CCAACCCCTG TAGTGCGCCT TCTATACTAG AAAGCTTGAC CACTGAGCCA CACCTCCCAC	1140
TAGTGCTTCA ATGTCAACCG AGAGTAAAAT GTGTTGTAT GAAATGCCTC CATTGACTA	1200
GATAGAGCTT TATTGGAGA AAGTCACATA TAACATAATT GAACTTTGAA TTATACAATC	1260
CCGTGGATTAGT TAGAGTGCTC CTGGAGCAGG TGGCAGTCAC CACTATCTAC TTCCAGAAC	1320
GTCTCATCCT TTCCAGAAAC CCACACTCTG TCTTCCTCT ATTCCAGATC TGTTAGACGA	1380
GTGGAATTAC ATAGTCCGGT CTTTCTGAG TTCTGTTACT AAGTTTAAA GGTTTATTCT	1440
CAGGTAGCAT CAGTCCGTAA TGTATTACTG CTGAATAGTG TTCCGTGTAT ACAGACACCG	1500
TGTGTGTCTT CTTCCAGCGA GCAGAGGAAC TCTGAGCTGT TTCTACTTTG GGGCTTTGA	1560
CTAATGCTAT GAACATCTGT GAAAAAGTTC GAAATGTTG ATTTAGTACA GACCCTAGTG	1620
GGGAGCTCCG GGGTCATATT ATGACAGCCT CAATTGTACT TCCTACAGTG GTTTACCAC	1680

CATTTCCCTGC TCTCGTGGGA TCTAGGCTCC AGCATCCCTC ACAACTTTCT GCCTGAGATG	1740
AAGAGGCATC TGATTGGAT CTTGGTTGC ATTTCCCTAA TGTCTAATAA TCTGAGCTTT	1800
TTTCATGTG TTCATGGCT TTCTATGCTG CTTTGAGAA TGTTTATTTC AGGCTACAGT	1860
CTGCCCTTCA GCTGGGTTAT CTTTCTGTTT TTCTGTAGGA TTTTTTATTTC ACGGTCAACT	1920
CATCTCTTAA AGATTAATTG GCATTTTTT TTTTCTCAAC TTGTGGTTTG CCCTCTCAA	1980
TGTCTTGATG CTCTCTGAAG CACAGTTTT ATTTCATATT ATTGCCTTTC TGCGTCTTAG	2040
CCCAGGCTGG CCAGGAATCC CCAAAGCCTT GTACACAGAG TGAGCATTTC CACCGCCTCA	2100
CTTCCCAGAA GGCACACGGC GCTGCTCCTG CCTAGAGCAG TTTTCATATT GGAAAATAAC	2160
AATGTGTTT TTCTTTCAGT GTATCCTAAC AAACCATTCC TAACCTGGAC TTACAGAAC	2220
TTATGCTTC ACTAAAGAAT TTTAAATT TACCTCTTAC CTGTAGGCCT GTGCTCTCAA	2280
AATGTTACAC ACCTTTATTC ATGCCATAT TTAAAATTAA GTAGAAATAG TGAGTATGTA	2340
GATATGCCCTG TATCGTGATG AGCACATTCA CAGTGCAGTG CAGTTGGCCT GCAGCCCCAGT	2400
TCTGCATCCA CCTCAGAAAA TGCCCAGTGA GCCCATCTAA TGACTCCAG CCCCTGCCAG	2460
GTCCTCCCTC CCTGCCCTGT CTTGGCATAAC TCTCTTCTCC ATGGCAATCA CCATTCTCTG	2520
TCCTGTTCT GAATTGAGT ACCCTAAGTG CCTGGTATAC ATAGATTCTC AGTGGGTGTG	2580
TGTGTGTGTG TGTGTGTGTG TGTGCGTGC TGTTCATGTA GCAGAATGCC GTGAAGGCTT	2640
GTATCATGTA TGAGTTTCCT TTGTAAGGAC AAATAGTACT TTAGACTTTA GTGTGTGTTG	2700
TATGTATGCT GTATGTTCT TGTTACCTAC TCATCCAGCC GTGGGTACCT CAGTTGTTCC	2760
CACCCCTGGAG CTCCCTGACTA TGCTGTGAAC ATGTATATAC AAATATCCCT CGGATCCTGC	2820
TTAGCATACA CGCAGCAGAT TGTATGCTT AGGGTAACCTC TGCTGTTATT AGTAGGCAC	2880
GCCGTAGTCT CCATAGTGAC CACACTATTG TATGTCCTGG CAGCAGTGCA CAGAGATTAG	2940
AAGTGCCCAT GTCCTTGTGA GTCTTACTCT TTTTTTAGTG GCTGTTCTAG TAGGTGTTAA	3000
GATCTGCTAG TGCTTCTGCT TCCCACCTCT CTGACTACTG ATGTCACATG TTTTATATGC	3060
TTGGTGGCCT TCTTTATATA TCGTTTGAAG AAATCTCTT AGGTCCACTG CCCATTAATA	3120
GTTGGGTCGT TGGCTCTGGT TGAATTTTTG GTAGTCACAT CCACAAAAGC ATTAACCCAC	3180
CCAAGGGAGC CTACTACAGC TTGCCCTAGG AAACCTGATT TTAGCTCTTA GCTTTGCTCT	3240
CTGGTATATT TTGAGTTCAT TTGTGTGTGA GATGTAAGGT CTGACTTTCT ACTCTACCCA	3300
TGTGGATACC TGGCTTTGCA TGTTGCCCTT GGTGGGAAAA CATCCCGCTG TGCATGGTGG	3360
GGCTGTTCT GAGCCTGGTC TCTTCCATGA CCTCTGTCTG CCTTCATGCC AACGCCACTG	3420
CTTTGATTAC TGGAGAATTA TAATAGAAAT TTGAAATCAG AAAATGTTG TTCTGTAATA	3480
AAAATTTGAA ATCAGAAAGT GTTCTATAAT AAAAATTGAA AATCAGAAAA A	3531

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HW037

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 280..1422

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1370..1796
 (D) OTHER INFORMATION: /label= SAC_24354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTGCGACCTGC GGCTGGCCGG CGGGGGCAGGC CCCGGACCCG	TGCGGGTTCCCT GGGCATGGTG	60
AGCAAGGGC TGCTGCGCCT TGTCTCTTCA GTCAACCGCA	GGAAGATGAA GCTTCTGCTG	120
GGCATCGCGC TGTTCGCCTA CGCCGCCTAA CTTGCTCATG	ATGGAGTGCC AAGTGCCTCA	180
GAGAACACAGG CCACCAGAAG AACAGTGCAT TCTCAGTACA	AGGGCAGCGT TCAGCATTG	240
GATATTGGAG TTGAAGCTGT TTGGGGCAAC TTTGTTAAC	ATG AGG TCT ATC CAG	294
	Met Arg Ser Ile Gln	
	1 5	
GAA AAT GGT GAA CTA AAG ATT GAA AGC AAG ATT GAA GAG ATT ATT GAA		342
Glu Asn Gly Glu Leu Lys Ile Glu Ser Lys Ile Glu Glu Ile Ile Glu		
10 15 20		
CCA TTA AGA GAG AAA ATC AGA GAT TTG GAA AAA AGT TTC ACC CAG AAA		390
Pro Leu Arg Glu Lys Ile Arg Asp Leu Glu Lys Ser Phe Thr Gln Lys		
25 30 35		
TAC CCA CCA GTA AAG TTT TTG TCA GAA AAG GAC CGG AAG AGG ATT TTG		438
Tyr Pro Pro Val Lys Phe Leu Ser Glu Lys Asp Arg Lys Arg Ile Leu		
40 45 50		
ATC ACT GGA GGT GCG GGC TTT GTG GGC TCC CAT CTA ACT GAC AAA CTC		486
Ile Thr Gly Gly Ala Gly Phe Val Gly Ser His Leu Thr Asp Lys Leu		
55 60 65		
ATG ATG GAT GGC CAT GAG GTG ACC GTG GTG GAC AAC TTC TTC ACA GGC		534
Met Met Asp Gly His Glu Val Thr Val Val Asp Asn Phe Phe Thr Gly		
70 75 80 85		
AGG AAG AGA AAT GTG GAA CAC TGG ATT GGC CAT GAG AAC TTC GAG CTG		582
Arg Lys Arg Asn Val Glu His Trp Ile Gly His Glu Asn Phe Glu Leu		
90 95 100		

ATT AAC CAT GAT GTG GTA GAG CCA CTC TAC ATC GAA GTT GAC CAG ATC Ile Asn His Asp Val Val Glu Pro Leu Tyr Ile Glu Val Asp Gln Ile 105 110 115	630
TAC CAT CTG GCT TCT CCA GCC TCC CCT CCA AAC TAC ATG TAC AAC CCC Tyr His Leu Ala Ser Pro Ala Ser Pro Pro Asn Tyr Met Tyr Asn Pro 120 125 130	678
ATC AAG ACC CTG AAG ACA AAT ACA ATT GGA ACA CTA AAC ATG TTG GGA Ile Lys Thr Leu Lys Thr Asn Thr Ile Gly Thr Leu Asn Met Leu Gly 135 140 145	726
CTG GCA AAG CGT GTG GGT GCC CGT CTG CTC CTA GCC TCC ACA TCT GAG Leu Ala Lys Arg Val Gly Ala Arg Leu Leu Ala Ser Thr Ser Glu 150 155 160 165	774
GTA TAT GGA GAT CCT GAG GTC CAC CCT CAA AGT GAG GAC TAC TGG GGC Val Tyr Gly Asp Pro Glu Val His Pro Gln Ser Glu Asp Tyr Trp Gly 170 175 180	822
CAC GTG AAT CCC ATA GGA CCC CGA GCC TGC TAT GAC GAG GGC AAA CGT His Val Asn Pro Ile Gly Pro Arg Ala Cys Tyr Asp Glu Gly Lys Arg 185 190 195	870
GTT GCG GAA ACC ATG TGC TAT GCC TAC ATG AAG CAG GAA GGT GTG GAG Val Ala Glu Thr Met Cys Tyr Ala Tyr Met Lys Gln Glu Gly Val Glu 200 205 210	918
GTG CGG GTG GCC AGG ATC TTC AAC ACC TTT GGG CCA CGA ATG CAC ATG Val Arg Val Ala Arg Ile Phe Asn Thr Phe Gly Pro Arg Met His Met 215 220 225	966
AAT GAT GGG AGG GTG GTC AGC AAC TTC ATC TTA CAA GCG CTA CAA GGG Asn Asp Gly Arg Val Val Ser Asn Phe Ile Leu Gln Ala Leu Gln Gly 230 235 240 245	1014
GAG CCG CTC ACA GTA TAT GGA TCT GGG TCT CAG ACA CGG GCA TTC CAG Glu Pro Leu Thr Val Tyr Gly Ser Gly Ser Gln Thr Arg Ala Phe Gln 250 255 260	1062
TAT GTT AGC GAT CTA GTG AAT GGC CTG GTA GCA CTG ATG AAC AGC AAT Tyr Val Ser Asp Leu Val Asn Gly Leu Val Ala Leu Met Asn Ser Asn 265 270 275	1110
GTC AGC AGC CCT GTC AAC CTG GGA AAT CCA GAA GAA CAC ACA ATC CTG Val Ser Ser Pro Val Asn Leu Gly Asn Pro Glu Glu His Thr Ile Leu 280 285 290	1158
GAA TTT GCT CAG TTA ATT AAA AAC CTT GTT GGT AGT GGA AGT GAA ATT Glu Phe Ala Gln Leu Ile Lys Asn Leu Val Gly Ser Gly Ser Glu Ile 295 300 305	1206
CAG TTT CTC TCT GAA GCT CAG GAT GAT CCA CAG AAA AGA AAA CCA GAC Gln Phe Leu Ser Glu Ala Gln Asp Asp Pro Gln Lys Arg Lys Pro Asp 310 315 320 325	1254
ATC AAA AAA GCA AAA CTG ATG CTG GGG TGG GAG CCT GTG GTT CCA TTG Ile Lys Lys Ala Lys Leu Met Leu Gly Trp Glu Pro Val Val Pro Leu 330 335 340	1302
GAG GAA GGA TTG AAC AAA GCC ATC CAC TAT TTC CCG AAG GAA CTA GAG Glu Glu Gly Leu Asn Lys Ala Ile His Tyr Phe Arg Lys Glu Leu Glu	1350

345	350	355	
TAC CAG GCT AAT AAC CAG TAC ATC CCT AAA CCC AAG CCT GCC AGA GTG Tyr Gln Ala Asn Asn Gln Tyr Ile Pro Lys Pro Lys Pro Ala Arg Val			1398
360	365	370	
AAG AAG GGC CGG ACG CGC CAC AGC TGAGTTAGCC TTGGGATGCG AGACTCTATT Lys Lys Gly Arg Thr Arg His Ser			1452
375	380		
TTACTTTATA AGGTGGACTT TTGTGGGATT TTTTTTTTT TTTTAAGACT TAAACAGGTG			1512
TCATGAAGAA CAAACTGGAA TTTTATTCTG AAGCTTGCTT TAAAGACACT GATGTGCCTA			1572
AAAGCTCCCT TGAACTCTGC AGACTTTGCC TTGCACTTTT TAACTCTGTC TTTTTTATGC			1632
ACAACAGCCT AGATGCATTC TCTGCTATTT TCAGGTTTT TTATCTTGCT GTTAGAGTGT			1692
ATGCTGTAAC TGTCACTGAC AGTTTTATTT ACTGGTTCT TTGTGAAGCT GAAAAGAAC			1752
ATTAAATGGG GTGGAAAATG CCAATTATTTAT TTATAAAAGT GAGTACTTTA TAAATGAGAT			1812
GTTACACTAT GCATAAAAGAA TACAAACCTA GAGGTATGGC CAGCTGGGCA GTGCACCAGT			1872
GTGTTATTGG GGACAGATGA AAGAACTCCA TTGGAAAGCT TTGCATTCT TTTTTAATTC			1932
TGAATTTCT GAAGGTCTAG TTTTCAGTTA CAGACTTGAC TTTGAAACAT CCCTGTTGGT			1992
TCTTGATCAA AGATATTTGA AATCACTACT GTGTTGTGCT GCATATTGGG GTGGGGTGG			2052
GGACAAATGTT AACATATTCT TGGTTAACCA TGGTTAAATA TGCTATTAA ATAAAATATT			2112
GAAACTCGTC AAAAA			2127

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

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Met Arg Ser Ile Gln Glu Asn Gly Glu Leu Lys Ile Glu Ser Lys Ile
 1           5           10          15

Glu Glu Ile Ile Glu Pro Leu Arg Glu Lys Ile Arg Asp Leu Glu Lys
 20          25           30

Ser Phe Thr Gln Lys Tyr Pro Pro Val Lys Phe Leu Ser Glu Lys Asp
 35          40           45

Arg Lys Arg Ile Leu Ile Thr Gly Gly Ala Gly Phe Val Gly Ser His
 50          55           60

Leu Thr Asp Lys Leu Met Met Asp Gly His Glu Val Thr Val Val Asp
 65          70           75          80

Asn Phe Phe Thr Gly Arg Lys Arg Asn Val Glu His Trp Ile Gly His
 85          90           95

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Glu Asn Phe Glu Leu Ile Asn His Asp Val Val Glu Pro Leu Tyr Ile
 100 105 110
 Glu Val Asp Gln Ile Tyr His Leu Ala Ser Pro Ala Ser Pro Pro Asn
 115 120 125
 Tyr Met Tyr Asn Pro Ile Lys Thr Leu Lys Thr Asn Thr Ile Gly Thr
 130 135 140
 Leu Asn Met Leu Gly Leu Ala Lys Arg Val Gly Ala Arg Leu Leu
 145 150 155 160
 Ala Ser Thr Ser Glu Val Tyr Gly Asp Pro Glu Val His Pro Gln Ser
 165 170 175
 Glu Asp Tyr Trp Gly His Val Asn Pro Ile Gly Pro Arg Ala Cys Tyr
 180 185 190
 Asp Glu Gly Lys Arg Val Ala Glu Thr Met Cys Tyr Ala Tyr Met Lys
 195 200 205
 Gln Glu Gly Val Glu Val Arg Val Ala Arg Ile Phe Asn Thr Phe Gly
 210 215 220
 Pro Arg Met His Met Asn Asp Gly Arg Val Val Ser Asn Phe Ile Leu
 225 230 235 240
 Gln Ala Leu Gln Gly Glu Pro Leu Thr Val Tyr Gly Ser Gly Ser Gln
 245 250 255
 Thr Arg Ala Phe Gln Tyr Val Ser Asp Leu Val Asn Gly Leu Val Ala
 260 265 270
 Leu Met Asn Ser Asn Val Ser Ser Pro Val Asn Leu Gly Asn Pro Glu
 275 280 285
 Glu His Thr Ile Leu Glu Phe Ala Gln Leu Ile Lys Asn Leu Val Gly
 290 295 300
 Ser Gly Ser Glu Ile Gln Phe Leu Ser Glu Ala Gln Asp Asp Pro Gln
 305 310 315 320
 Lys Arg Lys Pro Asp Ile Lys Lys Ala Lys Leu Met Leu Gly Trp Glu
 325 330 335
 Pro Val Val Pro Leu Glu Glu Gly Leu Asn Lys Ala Ile His Tyr Phe
 340 345 350
 Arg Lys Glu Leu Glu Tyr Gln Ala Asn Asn Gln Tyr Ile Pro Lys Pro
 355 360 365
 Lys Pro Ala Arg Val Lys Lys Gly Arg Thr Arg His Ser
 370 375 380

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1785 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HW038

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1440..1714

(D) OTHER INFORMATION: /label= SAC_24332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTGACGGTT GAGTCTGATG AGGAAGATCA AGAAAAGACT GAGGAGACTC CTTCCCAGCT	60
GGACCAGGAT ACTCAAGTAC AGGACATGGA TGAGGGTTCA GACGATGAAG AAGAAGGACA	120
GAAAGTGCCT CCACCCCCAG AGACACCCAT GCCTCCACCT CTGCCCCAA CACCAGACCA	180
AGTCATTGTG CGAAAGGACT ATGATCCAA AGCTTCCAAG CCCCTTCCTC CAGCTCCTGC	240
TCCTGATGAG TATCTTGTGT CCCCCATAAC TGGGGAGAAG ATTCCCTGCCA GCAAAATGCA	300
AGAACACATG CGCATCGGGC TTCTTGACCC CCGCTGGCTG GAGCAACGGG ATCGCTCCAT	360
CCGAGAGAAG CAGAGCANTG ATGAGGTGTA CGCACCCAGGT CTGGATATTG AGAGCAGCCT	420
AAAGCAGTTG GCTGAGCGAC GTACTGACAT CTTTGGGTA GAAGAGACAG CCATTGGTAA	480
GAAGATTGGT GAAGAGGAGA TCCAGAAGCC AGAGGAAAAG GTGACTTGGG ATGGCCATTC	540
AGGCAGCATG GCCCGGACCC AGCAGGCTGC CCAGGCCAAC ATCACCTCCA GGAGCAGATT	600
GAGGCCATCC ATAAGGCCAA GGGCTGGTG CCAGAAGATG ACACCAAAGA GAAGATTGGC	660
CCTAGCAAGC CCAATGAAAT CCCTCAGCAG CCACCGCTCC ATCTTCAGCC ACCAATATCC	720
CCAGCTCAGC GCCCCCCATC ACGTCATTCC CCGGCCACCT GCGATGCCAC CTCCAGTCCG	780
CACCACTGTC GTATCTGCAG TGCCTGTCAT GCCTGGCCC CCCATGGCAT CTGTGGTCCG	840
GCTGCCCTCA GGCTCAGTGA TTGCCCCAT GCCACCCATC ATCCACGCAC CTAGGATCAA	900
CGTGGTACCC ATGCCTCCTG CAGCACCNCC CATCATGGCA CCCGNCCAC CTCCCATGAT	960
TGTGCCAACCA GCCTTTGTGC CTGCTCCCC CTGTGGCTCC AGTGCCAGCC CCAGCTCCAA	1020
TGCCTCCCGT ACACCCCCCA CCTCCTATGG AAGATGAGCC TCCATCCAAG AAACATAAGA	1080
CCGAGGACAG CCTCATGCCT GAGGAAGAGT TCCTGCGCAG GAACAAGGGT CCAGTATCCA	1140
TCAAGGTGCA GGTACCCAAC ATGCAGGATA AGACAGAATG GAAGCTGAAT GGGCAGGGC	1200
TGGTCTTCAC TCTCCCGCTC ACAGACCAGG TCTCTGTCAT CAAAGTGAAG ATTCAAGGACT	1260
CNACGGGCAT GCCTGCAGGG AAGCAGAAC TACAGTATGA AGGCATCTTC ATCAAGGACT	1320
CCAACTCCCT GGCTTACTAC AACATGGCCA GTGGTGCTGT CATCCACTTG GCCCTCAAGG	1380

AAAGAGGCGG CCGGAAGAAG TAGCCTCGAG AGATACTGCA AGTGGACTCC TGCCATTGTA	1440
CCTCTTCCA CCACCAATTC CGGGAGTTTC CCTGGGACCT CGGGCACAGC CTGGGCATTT	1500
GTCTCCCTCT AAGGCAGTCT ATGGAATGGA TATCTGTTA GATTTGGATT GGAGGTCCCTT	1560
CAAGGAAGCC CATTAGGAAT TGAAAACCCA GGGTTCTCCC ACAGGAGAGC TTCATAATAC	1620
CAAGTAATGT TTGGCTAATA GAGTATGGTT ACTACCATT TCATTTGTGT ATCATGCTTT	1680
GGCCTCTAAT AAACCTCTTG AAGCCAGGCA TGGTACACAC ATGCCTGTAA TCCCAGGACT	1740
TGGGGGGCGG GCAGAAGAAT TAAATGTTCA TCTTGGCTGT AAAAAA	1785

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1054 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HW039

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 231..617
 (D) OTHER INFORMATION: /label= SAC_24045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TTTTTCAGAA TTGGCTGACT TTAATTTGGA AACAGCTTTT GGCTACAGAC ATTCAAGGTTT	60
AAGGCACATT CCAAACCTACA AGGATCCCTG CCACTGGCAC GGGGCCTGGC TTTAATTCTT	120
GCATGGTTTT ACATGGAAAG TGGAACAAAT GATTTCTGG CCTCTTCTAA AAAAGAGTGT	180
GAGTTGGCA AAAACAAAAC TCATGACACA TTCTCACCAG ACACCACAGT ACCGTTACAA	240
GACCTCCCTT TTGTCCTAGG CAAAGACGGG TGGCCCGCTC ACCTACCATT CTCTCCAGAA	300
ACATGTATAC AGTAAGCATG CTTGTATGCG TCTGTCTGGC AGCGATGGTT AAAAAAAAGTT	360
TTCAAATAAA AATACAAAAA TCACACGTCT ATAACAAAGC TAAGAGTCTT AGCCACAAGC	420
AGCGAGGAAT GAGTGTAGGA ACCAGGAGAG ATAAACATCA ATTCTGCACA GCAAGGGCT	480
GTGAGGGCCA GGGAGATGGT CACCTGAGAA CCTGGCCAC CTGGGCCCTT CGGCACAATA	540
CGTGGATGAG GGGGGACCAAG AAGGAAAAGG TCATGGCTTT GGGGATGGGT GGATGGCTGG	600
GGGGTGCAC TGTGGGTACT AGATAGATTG GGGAACTGG TGTGCTCTTC GGGACGTTTC	660

CTGGCCACTG CCAGCAGGGG GCCAGCAGGG GGCACAGGTG AGCCACTGCC ACCGCTCAGT	720
CGTTGCCACC ACAGATCTTC AGCAGGATCT TCCGATAATC CCCAGAAAGTG TCTCCCGTGA	780
TATCGTGGTA CAGTGACTTG CCGTACATCC GCTTATACTC TGCTCGGATA TCCAGCAGGT	840
CAAGCTCGCT TCGAGACACC ATGATGCGAA TCAGGGTCCG GTCTTTTGTGTT CCTGCTCCCC	900
CTCATAGCCT TGGTGGCCT TTCGGCAAAG AAGGCAGGGG TGTTCTTGAG GCATTTCACCC	960
ACAGCCAGCA TGCCCTGCTC CAGGTCCCCA GACATCTCCG GCAGATGCTC TTCTCGATGT	1020
CTCGGCCTGT CATCCTCTGA TACTCGTTGA AACT	1054

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3306 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HW040

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 481..2433

(xi) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: complement (2395..2588)
 (D) OTHER INFORMATION: /label= SAC_24520

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTCGACGCCT GGTGTGGCTG GCGGCACCAAG CTGAGTATTCTCTGAAAGAA TGAAGATGAC	60
TGGCCTAGAG GAGTCAGGAA TGTGACTGCT GGGAGATCCA GCTAGAGCAA CCATACCTGC	120
TTTTCCAGGA CCTTCCCCCT AACAGCTAACAG GAGCCTTAGG TCTGGGAGAG GCAGGCACCT	180
GGCTGCAGAA GGGGAAACAA CCTTTTCTC TTTCTCTCCT CCACTACTCT CCTGATGGCT	240
GCAGAAAGAAG AAAGATCTAC CACGGAAAC TCGGAGAGCT AGTCGGTTAA CTGAGCTGTT	300
GGATCTCCAC GGCACGAGGC AAATCCGTGA TGTGACTTTT TGTGAGGCT CCTAGGTCAG	360
CTGAGGAAAC AGCTCAGTTA CCTTAAGGGC GATAACTTTT TCAGGTTTAC TTGTGCCGAT	420
TGCTCGGCAG ACGGCAAGGA GCAGTCCGAG AGGCTGAAGC TGACATGGCA GCAAGTGGTC	480
ATG CTG GCT ATG TAC AAC TTG TCT CTG GAA GGA AGT GGA CGT CAA GGC	528
Met Leu Ala Met Tyr Asn Leu Ser Leu Glu Gly Ser Gly Arg Gln Gly	
1 5 10 15	
TAC TTC CGG TGG AAA GAA GAT ATC TGT GCT TTT ATT GAG AAA CAT TGG	576

Tyr Phe Arg Trp Lys Glu Asp Ile Cys Ala Phe Ile Glu Lys His Trp			
20	25	30	
ACT TTT TTA CTA GGA AAT AGG AAA AAG ACT TCG ACG TGG TGG AGC ACA		624	
Thr Phe Leu Leu Gly Asn Arg Lys Lys Thr Ser Thr Trp Trp Ser Thr			
35	40	45	
GTA GCA GGT TGC CTC AGC GTG GGA AGT CCT GTT TAT TTC CGT TCA GGT		672	
Val Ala Gly Cys Leu Ser Val Gly Ser Pro Val Tyr Phe Arg Ser Gly			
50	55	60	
GCT CAG GAA TTT GGA GAG CCT GGA TGG TGG AAA CTT GTT CAT AAC AGA		720	
Ala Gln Glu Phe Gly Glu Pro Gly Trp Trp Lys Leu Val His Asn Arg			
65	70	75	80
CCC CCA ACA ATG AGA CCA GAG GGA GAG AAG CTG TCT GCC TCC ACT TTG		768	
Pro Pro Thr Met Arg Pro Glu Gly Glu Lys Leu Ser Ala Ser Thr Leu			
85	90	95	
AAA GTG AAA GCT TCA AAA CCA ACA CTG GAT CCC ATC ATT ACC GTT GAA		816	
Lys Val Lys Ala Ser Lys Pro Thr Leu Asp Pro Ile Ile Thr Val Glu			
100	105	110	
GGA CTC AGA AAA CGA GCA AGC CGG AAT CCT GTG GAA TCA GCC ATG GAA		864	
Gly Leu Arg Lys Arg Ala Ser Arg Asn Pro Val Glu Ser Ala Met Glu			
115	120	125	
TTG AAA GAG AAG CGG TCT CGA ACA CAG GAA GCT AAA GAC ATC AGA AGA		912	
Leu Lys Glu Lys Arg Ser Arg Thr Gln Glu Ala Lys Asp Ile Arg Arg			
130	135	140	
GCA CAG AAA GAA GCA GCC GGC CTC CTT GAC AGA AGC ACC TCT TCT ACC		960	
Ala Gln Lys Glu Ala Ala Gly Leu Leu Asp Arg Ser Thr Ser Ser Thr			
145	150	155	160
CCT GTC AAG TTC ATA AGC CGA GGC CGG AGG CCG GAT ATG ATT TTG GAG		1008	
Pro Val Lys Phe Ile Ser Arg Gly Arg Arg Pro Asp Met Ile Leu Glu			
165	170	175	
AAA GGA GAA GTG ATT GAC TTT TCA TCC CTG AGC TCC TCG GAC CGT ACC		1056	
Lys Gly Glu Val Ile Asp Phe Ser Ser Leu Ser Ser Ser Asp Arg Thr			
180	185	190	
CCC CTC ACA AGC CCC TCT CCT TCT CCC TCT CTG GAT TTC TCT GCC CCA		1104	
Pro Leu Thr Ser Pro Ser Pro Ser Pro Ser Leu Asp Phe Ser Ala Pro			
195	200	205	
GGG ACA CCA GCG TCA CAT TCT GCC ACG CCT AGC TTG CTC TCT GAA GCA		1152	
Gly Thr Pro Ala Ser His Ser Ala Thr Pro Ser Leu Leu Ser Glu Ala			
210	215	220	
GAC CTC ATC CCA GAC GTG ATG CCA CCC CAA GCT CTA TTT CAT GAT GAT		1200	
Asp Leu Ile Pro Asp Val Met Pro Pro Gln Ala Leu Phe His Asp Asp			
225	230	235	240
GAT GAG CTG GAA GGA GAT GGA GTC ATA GAC CCA GGG ATG GAG TAC ATC		1248	
Asp Glu Leu Glu Gly Asp Gly Val Ile Asp Pro Gly Met Glu Tyr Ile			
245	250	255	
CCA CCC CCA GCT GGG TCA GCT TCT GGG CTG ATG GGG AGC AGA AAG AAG		1296	
Pro Pro Pro Ala Gly Ser Ala Ser Gly Leu Met Gly Ser Arg Lys Lys			
260	265	270	

GTC AGA GCT GCA GAG CAG ATA AAA CAG GAA GTC GAC AGC GAG GAG GAG Val Arg Ala Ala Glu Gln Ile Lys Gln Glu Val Asp Ser Glu Glu Glu 275 280 285	1344
AAG CCA GAC AGG ATG GAT GGA GAT AGC GAA GAC ACA GAT TCA AAC ACT Lys Pro Asp Arg Met Asp Gly Asp Ser Glu Asp Thr Asp Ser Asn Thr 290 295 300	1392
TCT TTG CAC ACT AGA GCT CGA GAA AAG AGG AAG CCA CCC CTG GAG AAG Ser Leu His Thr Arg Ala Arg Glu Lys Arg Lys Pro Pro Leu Glu Lys 305 310 315 320	1440
GAC ACG AAG CCC AAG GGG CCC AGG TAT ACG CCT GTG AGC ATC TAT GAG Asp Thr Lys Pro Lys Gly Pro Arg Tyr Thr Pro Val Ser Ile Tyr Glu 325 330 335	1488
GAG AAG CTG CTG CTC AAG AGG CTG GAG GCA TGC CCT GGT GCC GTG GCC Glu Lys Leu Leu Lys Arg Leu Glu Ala Cys Pro Gly Ala Val Ala 340 345 350	1536
ATG ACT CCA GAA GCC CGG AGG CTG AAA CGG AAG CTG ATC GTC CGG CAA Met Thr Pro Glu Ala Arg Arg Leu Lys Arg Lys Leu Ile Val Arg Gln 355 360 365	1584
GCA AAA AGG GAT CGG GGC TTA CCA CTG TTT GAC TTG GAC GAG GTT GTG Ala Lys Arg Asp Arg Gly Leu Pro Leu Phe Asp Leu Asp Glu Val Val 370 375 380	1632
AAC GCA GCA CTT CTG TTA GTG GAT GGG ATT TAT GGA GCC AAA GAT GGA Asn Ala Ala Leu Leu Val Asp Gly Ile Tyr Gly Ala Lys Asp Gly 385 390 395 400	1680
GGA GCT TCC CGG CTT CCA GCT GGA CAA GCT ACA TAC CGG ACC ACC TGC Gly Ala Ser Arg Leu Pro Ala Gly Gln Ala Thr Tyr Arg Thr Thr Cys 405 410 415	1728
CAG GAC TTC AGG ATC CTT GAC CGG TAC CAG ACT GCC TTA CCA GCC AGG Gln Asp Phe Arg Ile Leu Asp Arg Tyr Gln Thr Ala Leu Pro Ala Arg 420 425 430	1776
AAA GGA TTC CGG CAC CAG ACC ACC AGA TTT TTG TAT CGT CTG GTG GGA Lys Gly Phe Arg His Gln Thr Thr Arg Phe Leu Tyr Arg Leu Val Gly 435 440 445	1824
TCA GAA GAT CTG GCT GTG GAC CAA AGT ATT GTC AGC CCT TAC ACT TCT Ser Glu Asp Leu Ala Val Asp Gln Ser Ile Val Ser Pro Tyr Thr Ser 450 455 460	1872
CGG ATC TTG AAA CCT TAT ATC AGG CGT GAT TAT GAG ACA AAG CCA CCC Arg Ile Leu Lys Pro Tyr Ile Arg Arg Asp Tyr Glu Thr Lys Pro Pro 465 470 475 480	1920
AAA CTA CAG CTG CTG TCC CAG ATT CGC TCC CAC CTG CAC AAG AGT GAC Lys Leu Gln Leu Ser Gln Ile Arg Ser His Leu His Lys Ser Asp 485 490 495	1968
CCT CAC TGG ACA CCT GAA CCT GAT GCA CCT CTC GAT TAC TGC TAT GTC Pro His Trp Thr Pro Glu Pro Asp Ala Pro Leu Asp Tyr Cys Tyr Val 500 505 510	2016
CGA CCA AAT CAC ATC CCA ACG ATC AAC TCC ATG TGT CAG GAA TTT TTC Arg Pro Asn His Ile Pro Thr Ile Asn Ser Met Cys Gln Glu Phe Phe 515 520 525	2064

TGG CCT GGC ATT GAC CTG TCT GAG TGT CTG CAG TAT CCA GAC TTC AGT Trp Pro Gly Ile Asp Leu Ser Glu Cys Leu Gln Tyr Pro Asp Phe Ser 530 535 540	2112
GTC GTA GTC CTT TAT AAA AAA GTC ATT GTT GCC TTT GGC TTC ATG GTT Val Val Val Leu Tyr Lys Lys Val Ile Val Ala Phe Gly Phe Met Val 545 550 555 560	2160
CCC GAT GTG AAG TAC AAC GAA GCT TAC ATT TCA TTT CTG CTT GTT CAT Pro Asp Val Lys Tyr Asn Glu Ala Tyr Ile Ser Phe Leu Leu Val His 565 570 575	2208
CCC GAG TGG AGG AGA GCA GGG ATT GCC ACG TTC ATG ATC TAT CAT CTG Pro Glu Trp Arg Arg Ala Gly Ile Ala Thr Phe Met Ile Tyr His Leu 580 585 590	2256
ATT CAG ACG TGC ATG GGC AAG GAT GTG ACT CTT CAC GTC TCG GCG AGC Ile Gln Thr Cys Met Gly Lys Asp Val Thr Leu His Val Ser Ala Ser 595 600 605	2304
AAC CCT GCC ATG CTG CTG TAC CAG AAG TTT GGC TTC AAG ACA GAG GAG Asn Pro Ala Met Leu Leu Tyr Gln Lys Phe Gly Phe Lys Thr Glu Glu 610 615 620	2352
TAT GTT TTG GAT TTT TAT GAT AAG TAT TAC CCA CTG GAG AGT ACA GAG Tyr Val Leu Asp Phe Tyr Asp Lys Tyr Tyr Pro Leu Glu Ser Thr Glu 625 630 635 640	2400
TGT AAA CAT GCA TTC TTC CTG AGG CTC CGA CGC TGAGGTGAAC TCAGTTCTTC Cys Lys His Ala Phe Phe Leu Arg Leu Arg Arg 645 650	2453
CCAGCAAACA GCAGATGCTG TCAGAGAGTG GCCTCAGAACAG TCGTGCAGGC CCTTCTCCTC GAAGTGGGCC CTGGCCTCCT GTGAGTAATG GCCTCCACAG GGTCCAGCTG GGTGAGTGAA GCCATGTGCA GAGGTACAAG TGGCTGTTCA ATCCAGAAC CATCCAGCAG GCCCTGCGTG GCCTTCCAGC AGTATCTTGG ACTCCACTGT GGACCAGAAC CAAGTGACTC TGCCATTCTT TTTCCACACA ATGAGTGGGC ACAAAAGAGC TTCTGAGCTG AAGCATTGA GAATGGCCT GCTCCTCCTA TGTGAGAGCT CAGGAAGTAT GAAAGATGTT AAAGACTGCC AGGGCCCTCA CTGTCCTGGG CCGAGAGGTT ATGAGGTGTC AGGAATGACT CCAACCTGT CTCAGCCTGT GCTGTGCTGT CATCGAACCC CAGAGGATTG ATGGGGCACT GAAGTCCTTT TGTCTCTTAC TGACTTTCTA CCTGGTCAGCA CCCCTTGCAG GGACATTGAC CTGGTACAAG AAGTTTACTC TTGGCATGGC CTGGAAAGTA GCCCCGAGAGG AACGGTTGAG CTTGATAACAT TAGATGCCCT CCCAGGCCCT TCTCATGCTC AGGACAGTTG CACCACAGAA GTGGAGGTGT GGAATGGCGC AGGCAGGCCCT GGGCGCCCTG TCCACCTCAT GAAGCTGCTT CCTGGGTTGC ACATGTTGGA GTTGGACTAC AGGTATCTAA GTGCATTCCA AAAGCATCAG ATATCTCCAA TAAAAATCCT TACCATACAA AAA	2513 2573 2633 2693 2753 2813 2873 2933 2993 3053 3113 3173 3233 3293 3306

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met	Leu	Ala	Met	Tyr	Asn	Leu	Ser	Leu	Glu	Gly	Ser	Gly	Arg	Gln	Gly
1					5			10					15		
Tyr	Phe	Arg	Trp	Lys	Glu	Asp	Ile	Cys	Ala	Phe	Ile	Glu	Lys	His	Trp
	20					25						30			
Thr	Phe	Leu	Leu	Gly	Asn	Arg	Lys	Lys	Thr	Ser	Thr	Trp	Trp	Ser	Thr
	35						40				45				
Val	Ala	Gly	Cys	Leu	Ser	Val	Gly	Ser	Pro	Val	Tyr	Phe	Arg	Ser	Gly
	50					55				60					
Ala	Gln	Glu	Phe	Gly	Glu	Pro	Gly	Trp	Trp	Lys	Leu	Val	His	Asn	Arg
	65					70				75				80	
Pro	Pro	Thr	Met	Arg	Pro	Glu	Gly	Glu	Lys	Leu	Ser	Ala	Ser	Thr	Leu
		85					90					95			
Lys	Val	Lys	Ala	Ser	Lys	Pro	Thr	Leu	Asp	Pro	Ile	Ile	Thr	Val	Glu
	100					105						110			
Gly	Leu	Arg	Lys	Arg	Ala	Ser	Arg	Asn	Pro	Val	Glu	Ser	Ala	Met	Glu
	115					120					125				
Leu	Lys	Glu	Lys	Arg	Ser	Arg	Thr	Gln	Glu	Ala	Lys	Asp	Ile	Arg	Arg
	130					135				140					
Ala	Gln	Lys	Glu	Ala	Ala	Gly	Leu	Leu	Asp	Arg	Ser	Thr	Ser	Ser	Thr
	145					150				155				160	
Pro	Val	Lys	Phe	Ile	Ser	Arg	Gly	Arg	Arg	Pro	Asp	Met	Ile	Leu	Glu
		165				170					175				
Lys	Gly	Glu	Val	Ile	Asp	Phe	Ser	Ser	Leu	Ser	Ser	Ser	Asp	Arg	Thr
	180				185						190				
Pro	Leu	Thr	Ser	Pro	Ser	Pro	Ser	Leu	Asp	Phe	Ser	Ala	Pro		
	195				200						205				
Gly	Thr	Pro	Ala	Ser	His	Ser	Ala	Thr	Pro	Ser	Leu	Leu	Ser	Glu	Ala
	210					215					220				
Asp	Leu	Ile	Pro	Asp	Val	Met	Pro	Pro	Gln	Ala	Leu	Phe	His	Asp	Asp
	225				230					235				240	
Asp	Glu	Leu	Glu	Gly	Asp	Gly	Val	Ile	Asp	Pro	Gly	Met	Glu	Tyr	Ile
	245					250					255				
Pro	Pro	Pro	Ala	Gly	Ser	Ala	Ser	Gly	Leu	Met	Gly	Ser	Arg	Lys	Lys
	260					265					270				

Val Arg Ala Ala Glu Gln Ile Lys Gln Glu Val Asp Ser Glu Glu Glu
 275 280 285
 Lys Pro Asp Arg Met Asp Gly Asp Ser Glu Asp Thr Asp Ser Asn Thr
 290 295 300
 Ser Leu His Thr Arg Ala Arg Glu Lys Arg Lys Pro Pro Leu Glu Lys
 305 310 315 320
 Asp Thr Lys Pro Lys Gly Pro Arg Tyr Thr Pro Val Ser Ile Tyr Glu
 325 330 335
 Glu Lys Leu Leu Leu Lys Arg Leu Glu Ala Cys Pro Gly Ala Val Ala
 340 345 350
 Met Thr Pro Glu Ala Arg Arg Leu Lys Arg Lys Leu Ile Val Arg Gln
 355 360 365
 Ala Lys Arg Asp Arg Gly Leu Pro Leu Phe Asp Leu Asp Glu Val Val
 370 375 380
 Asn Ala Ala Leu Leu Leu Val Asp Gly Ile Tyr Gly Ala Lys Asp Gly
 385 390 395 400
 Gly Ala Ser Arg Leu Pro Ala Gly Gln Ala Thr Tyr Arg Thr Thr Cys
 405 410 415
 Gln Asp Phe Arg Ile Leu Asp Arg Tyr Gln Thr Ala Leu Pro Ala Arg
 420 425 430
 Lys Gly Phe Arg His Gln Thr Thr Arg Phe Leu Tyr Arg Leu Val Gly
 435 440 445
 Ser Glu Asp Leu Ala Val Asp Gln Ser Ile Val Ser Pro Tyr Thr Ser
 450 455 460
 Arg Ile Leu Lys Pro Tyr Ile Arg Arg Asp Tyr Glu Thr Lys Pro Pro
 465 470 475 480
 Lys Leu Gln Leu Leu Ser Gln Ile Arg Ser His Leu His Lys Ser Asp
 485 490 495
 Pro His Trp Thr Pro Glu Pro Asp Ala Pro Leu Asp Tyr Cys Tyr Val
 500 505 510
 Arg Pro Asn His Ile Pro Thr Ile Asn Ser Met Cys Gln Glu Phe Phe
 515 520 525
 Trp Pro Gly Ile Asp Leu Ser Glu Cys Leu Gln Tyr Pro Asp Phe Ser
 530 535 540
 Val Val Val Leu Tyr Lys Lys Val Ile Val Ala Phe Gly Phe Met Val
 545 550 555 560
 Pro Asp Val Lys Tyr Asn Glu Ala Tyr Ile Ser Phe Leu Leu Val His
 565 570 575
 Pro Glu Trp Arg Arg Ala Gly Ile Ala Thr Phe Met Ile Tyr His Leu
 580 585 590
 Ile Gln Thr Cys Met Gly Lys Asp Val Thr Leu His Val Ser Ala Ser
 595 600 605

Asn Pro Ala Met Leu Leu Tyr Gln Lys Phe Gly Phe Lys Thr Glu Glu
 610 615 620

Tyr Val Leu Asp Phe Tyr Asp Lys Tyr Tyr Pro Leu Glu Ser Thr Glu
 625 630 635 640

Cys Lys His Ala Phe Phe Leu Arg Leu Arg Arg
 645 650

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HW041

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 3407..3482
- (D) OTHER INFORMATION: /label= SAC_24317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTCGACCCCTC CTTCTGCCCT GGCTCCTGTT GATGAGCACA GTGCCGTCCC TGATCAGTTC	60
TTTCTTCCTG TGAATTTGCT TCGTAGCCCA TCAGGGCTGGT AGACTGGCAG CACGGTCAGT	120
GTCACACGAG GGACAGGACT TCCCTGAAGT GAAGCAGCAA TGTATGGAA GCAAACCCCT	180
GTGAGCGAGA GACAGGCCCC GAGGCTGCTG CCACAAGGTC TCATGTTCAT TGCTGGGAC	240
ACTAGCTTCC TACAAACCCC AGGAGACGCT GCCCATAGCA CGGGTGGCCC TTCAGGCTCC	300
TGAACTATCT ATCCCCAGAT CAGTAGGATT TGTGTTCCAA GTCCCCCTTC TCATTCCCTC	360
TTTGCTCAAG AGAAAAAAAGA AAAGTGGTAA CTCTGTGACT CTAAGTCCCT CTTAAATGCA	420
GCGCTGAATC TAGCTTGGCT CGGAGATCTC TGACTTGTCC CTAGGGTGAG ACTGTGCCT	480
CCCCAGGTTG AGGTGGCACG TGTATTGTGA GAGATTAGCC TGGAGAGCAG AGAAGGGGG	540
AGGGGGGATA GGGAGGAGAG AGCAATCGTG TCTCCCTACA GGACCCCTGGG CCATCTGACA	600
AGACAGAGGA GGTGGGACTG GCTTCCCCAT GCTGCACATG GCAGTGGAA CCAGGCTTGG	660
AGTCCCCCAC CCCCTCCTTA CCTCTTCTCT CAGACCTTGT AGCCCTAGCT TGCCCTGTGC	720
TCTGCAGGGA AGGGGATGAG AGGACAGCAT AAGAACGTCTT GCCAGTTGAG GTGGGGCTGG	780
AAGATGAAGC AGGTGGGTGT AGGAATCATT TTGGATAGGG CATGTTGTTT GGTTGACGGC	840
AACTAATTCT CTTAAGAGCA TATTGCTCC AGTTAATGTT GGAGACAACC CAGAAAGGGA	900

AGGGTATAGA GATGGGTAAT TAATGAGATA TTCCAGCCCT GGAGCAATGT CTGAGCCACC	960
CCAAACTTAG GCTGTCTCCC AGCATAGGAG TGGGGCACTG CCCCTTACTC AAATTCTAGT	1020
CTAAGTGTTC CAGACACATT GTACACTTGG ACAGGAAATC TCCTGTTCCA GCATACCCCTC	1080
TCCCCCATAC CCTCTCCCCC ATACCCCTC CCCCATACCT TCTCCCCCAT ACTGTTAGTA	1140
CGTTTCAGTT GTTCAAAAGC AAAGGGGGCG CAGACTAGGC TTTAACTGCA TGTGGAGTGT	1200
AGATTTGCC TAAGAATCCA TGTTGAAGAA GAGAGAGGCT ATGTCTTTAA GGTGGAGGCC	1260
CTTCAGTCTT CTGTCCTTGT AATTCTCTTG AAGCGTGAGC CCCAGGCACT CAGAACCCAT	1320
GTTGTACTCC GGGAAAGTCA TGGGACCTGA ACTCCTCAA CACCGGGAAC AACAGTACTG	1380
CATAGGTACT TTGGTACTGA CTGTGCAAGC ACTAGAAAAA GTACCCGTTG AATGGCCCTC	1440
ACAGCATCAG GGAAACGAGG CCGAGTTCAC TCTCCTGATT GTCAGATGC AGAACGCTGGA	1500
CCCCTGAGGT GTACCAGCCC ACCTCCAAGC TTGACACAGA GGCTAGCACT TAAACCAAAG	1560
ACTCAGAAGA GGAGTCTCAG TCACAGGCTG CACAGCCTTG AACATGATAT CTAGAACTAT	1620
GCCTGGTGA TCGGTGGCCC AACTTGTGAC ACTTGTGTGC ACATAGGGAA GCTGACGCTC	1680
CTCTCGGGC CTGAAAACAG GACTAAACCC AAACCCATA TAACTAACCA TACCACTGCC	1740
ATCCACAGGC GTGGATGGAA GTCTTCACGG TCTGTTACAA GCACAAGTAC AAAGCCGATA	1800
AAAATAAGTC AAAGCCCTTC CTCGTGGTGC AGAGGGCTCC TCCTCAGATC TCTTGGAGCC	1860
TTTGATCATA GAGCTTGACG GTCTCCTCTC GGGATAAAGG ACAGGTAAAG GCTGTGGCCT	1920
TCAGCGGTGA CTGCCCCACA CCCTGCTTTC CTTAGGGGTG GAGACAAGGA ATGGTGGGGC	1980
CAGTGGTGT CAGAGAGAAG TCTCTCTTG GAGCCCATGT ATGGGGCTTG ACCTTTGCT	2040
GTGAGTGCAT TTAGAGGCAA GTGAATTCTG GCCTCAGTAC AGAGAACCCCA GCGGTTTCAG	2100
CACTCAAGAA AGAAGCCGCA GTGTCCCCTA CAGAGAGGCT CTGTCCTGCT TGGCCCCAGC	2160
CACCTGCGCC ACACATTAA TAAAGTGGCT GAAACTCCTC CTTTCCAAGA GCTAGTGTGC	2220
TGGGTCTGT CCTCCCCACA GCCTTCTGAG TCCCAGAGAC TTGTGTGAGC AGTCGGATAA	2280
GGCCAATCTG GGAGACAGGG GATGACCATG ACACAAGGTG TTTCCAGGCA GGTCCCTTGT	2340
GCGTAGGCTG CAGAGAGCTG TCCTGACTGG GAGCTGGGT TGTACGAACA CATGGTGCCT	2400
TCTTGTCTG TGCTGAACGA GTAGGGTGTG TTTCTCTGTG TTCTCTGAGT AAGATCACAC	2460
CCTCTTTAAG CAAAGGGGTG TTGTGGATAT TAGAAGCAAG ATTGATAAAT GTTCTAAAT	2520
GGTGGTGCTA GAGAAAAGTC AGTCCCCGTA ACTTCCTAAA AGCTGAGTCA GCCAGTCTCT	2580
AAGTATGTAC ATGTTGGCTT TCTTCTATTT TTTTCTAGT TAATCAGTGT GTTTAAATG	2640
TTTTTAGTTG ATGTGAGGAT TTTTTAAAG GCATTTGTGT GTGGTGTGGC TCCATGGGAG	2700
ATAGGCTGTG TAATAAGAAC CCTCAGAAC CAGCCAGTCA TCCAAGGGC GCCCAAGTTC	2760
AGTGGATTTC TTCAGGAATT GGAGAGCAGT ATTTTCCCT CTTTCAGTA GTATGCCTGT	2820

TCTCATTTAG TAATTTAATG GTATATTGCA TTATATGTGA ATGCATAACAT AAACGGTGGA	2880
ATTTCTCTTA ATATCCAAA AAGTCCTTCT GTGCCCTCT GAGCTCTCTC CTTGGGGAGG	2940
ACTGCAGGGC TCACGTGTA AAATGGTTGT GGACTCCTCT AGCAGAACATGG CTTCCAAGGC	3000
CTGGCCCATT CCTCAGATTG CCTTTGAAGT GAGAGGTCAT TGTCTTTGA GAATGGATT	3060
AAGTTTGAA AATACCCAC GCTGTTACA GTGCAAGCGA CTGAACACAG ACAATTAGT	3120
CAGAACATGAGA ATCCCAGGGC CATCAAGATG ACTCCACGGA AAAGGGACTG CCACCAACCA	3180
GAGCCAAGAC CTGAGTTGG TCCCCAGGAA CCCCATGGCA GCAGGAGAGA GTCAGCCGAT	3240
GCAAGTGTCA CACACACACA TAAACACACA CATAACACATG CAACACATAC ACACAAACAC	3300
ATACATACAC ACACACAAAC ACATACACAC ATGCACACAC ACACACACAC ACACACACAC	3360
AGAGTTTTG GAAGAATATC TATGATGTAG GAAAAGGTTT GTTAGTACCT GCAACCTCTA	3420
GGGCCTCATT TCCAAGCCTG CTGCTTCTCT TGCCAGGACT TATACGTGTG CAACCCCTGC	3480
GTACACTACA GACCTAAGTA CATACTCGCT AACATGAACA CCCAGTAGGT ATTCTGTAAA	3540
ACGGATATAC TTAAGTGCAT GTTATTGTCG TGTGTGCCGC GACTGAGCTG TGTCTTTGTC	3600
ATGAAACTTT GCTTCTTTGC CAAATTAAGA CTCTGCCCTC CCTCCGAGGA AGGAAATATA	3660
CAGCAGTTTC TCCAATCAGC TTCTCAAGTT TTCCCCCCTG TGTGTGTGTTT ACTTGTGGCT	3720
TTGCCTGAGA GTCTGTCCTC ACGTACACAC CTGTGAGTAT TTATTACAAG GCAGAACGGG	3780
GACAGGCGTA GCCATAGTAC TTGTGTTGA ATGTTCCAG GGAGGGACAA TGGAGCCCC	3840
TCCTCAGTGA GGTGCTCACA GAATCTGTGT CAAATTCTGT GAACGGGGTC CAACACTAGT	3900
ACCAGCTTCA CCCCCAACCT GAGTGCCCTG GAGCCACTGC CCTCTCTACT GCCTTGTGTG	3960
TGCATGGGTG TGGTTGTGTG TGTCTCTGTT GGGGCATGTG CGCATTTCG CAGTGGACTT	4020
TGGTATCCAC ATGTAACCTT TGGCATCTGT GTTCCCTGGAC CGCATTGACA GATCTGTGGT	4080
GTGCAGATCT GTGTAGATGG GTCTGTGTG AAAGTGGGGAA GTCCCCCTGAA AGTGAATATG	4140
GATATTGTTG GTCAGCCAAA GACTTTCTTA TTCTTGCTG CTTAAACTTT GTGCCTTAAT	4200
ATTGTAAATA TAAACGGTTA AAACAAAAGT CGAC	4234

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1792 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HW042

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 8..889

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: complement (1409..1618)
(D) OTHER INFORMATION: /label= SAC_24017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTCGACC AAG GAT GGT GGA AGT TTC AGT GGT ACT GGT GGC CTT CCA GAT	49
Lys Asp Gly Gly Ser Phe Ser Gly Thr Gly Gly Leu Pro Asp	
1 5 10	
TAT TCT GCC CCC AAT CCC ATT AAA GTG ACC CAT CGG TGC TAC ATC CTT	97
Tyr Ser Ala Pro Asn Pro Ile Lys Val Thr His Arg Cys Tyr Ile Leu	
15 20 25 30	
GAG AAT GAC ACA GTC CAG TGT GAC TTG GAC CTG TAC AAG TCC CTG CAG	145
Glu Asn Asp Thr Val Gln Cys Asp Leu Asp Leu Tyr Lys Ser Leu Gln	
35 40 45	
GCT TGG AAA GAC CAC AAA TTG CAC ATC GAC CAT GAG ATT GAA ACC CTG	193
Ala Trp Lys Asp His Lys Leu His Ile Asp His Glu Ile Glu Thr Leu	
50 55 60	
CAG AAC AAA ATT AAG AAC CTT CGA GAA GTC AGG GGT CAC CTG AAG AAG	241
Gln Asn Lys Ile Lys Asn Leu Arg Glu Val Arg Gly His Leu Lys Lys	
65 70 75	
AAG CGG CCA GAA GAA TGT GAC TGT CAC AAA GTC AGT TAC CAC AGC CAA	289
Lys Arg Pro Glu Glu Cys Asp Cys His Lys Val Ser Tyr His Ser Gln	
80 85 90	
CAC AAA GGC CGC CTC AAG CAC AAG GGC TCC AGC CTG CAC CCT TTC AGG	337
His Lys Gly Arg Leu Lys His Lys Gly Ser Ser Leu His Pro Phe Arg	
95 100 105 110	
AAG GGT CTG CAG GAG AAA GAC AAG GTG TGG CTG TTG CGG GAG CAG AAA	385
Lys Gly Leu Gln Glu Lys Asp Lys Val Trp Leu Leu Arg Glu Gln Lys	
115 120 125	
CGC AAG AAG AAA CTG CGC AAG CTG CTG AAG CGA CTG CAG AAC AAT GAC	433
Arg Lys Lys Leu Arg Lys Leu Leu Lys Arg Leu Gln Asn Asn Asp	
130 135 140	
ACG TGC AGC ATG CCG GGC CTC ACG TGC TTT ACT CAC GAC AAC CAC CAC	481
Thr Cys Ser Met Pro Gly Leu Thr Cys Phe Thr His Asp Asn His His	
145 150 155	
TGG CAG ACC GCG CCG CTC TGG ACG TTG GGA CCC TTC TGC GCC TGC ACC	529
Trp Gln Thr Ala Pro Leu Trp Thr Leu Gly Pro Phe Cys Ala Cys Thr	
160 165 170	
AGC GCC AAC AAT AAC ACG TAC TGG TGC CTG CGG ACC ATC AAC GAG ACC	577
Ser Ala Asn Asn Asn Thr Tyr Trp Cys Leu Arg Thr Ile Asn Glu Thr	
175 180 185 190	
CAC AAC TTC CTC TTC TGT GAA TTC GCA ACT GGC TTC ATA GAA TAC TTT	625

His Asn Phe Leu Phe Cys Glu Phe Ala Thr Gly Phe Ile Glu Tyr Phe		
195	200	205
GAC CTC AGT ACG GAC CCC TAC CAG CTG ATG AAC GCG GTC AAC ACA CTG		
Asp L u Ser Thr Asp Pro Tyr Gln Leu Met Asn Ala Val Asn Thr Leu		
210	215	220
GAC AGG GAC GTT CTC AAC CAG CTG CAC GTC CAG CTC ATG GAG CTA AGG		
Asp Arg Asp Val Leu Asn Gln Leu His Val Gln Leu Met Glu Leu Arg		
225	230	235
AGC TGC AAA GGC TAC AAG CAG TGT AAC CCC CGG ACC CGC AAT ATG GAC		
Ser Cys Lys Gly Tyr Lys Gln Cys Asn Pro Arg Thr Arg Asn Met Asp		
240	245	250
CTG GGG CTT AGA GAC GGA GGA AGC TAT GAG CAA TAC AGG CAG TTT CAG		
Leu Gly Leu Arg Asp Gly Gly Ser Tyr Glu Gln Tyr Arg Gln Phe Gln		
255	260	265
CGT CGA AAA TGG CCA GAA ATG AAG AGA CCC TCT TCC AAA TCA CTG GGA		
Arg Arg Lys Trp Pro Glu Met Lys Arg Pro Ser Ser Lys Ser Leu Gly		
275	280	285
CAG CTA TGG GAA GGT TGG GAA GGC TAATCGGCCA TGGAGAGGAA CCTCCAAAAC		
Gln Leu Trp Glu Gly Trp Glu Gly		
290		
CAGAGGCCCTC CTGTGGCTGC CCAGGCGTGC AAAAATCACC CAATTCCGAG GAGATCGATG		
CTGGAACTGG GAGACTTGAC AGGAGGCAGG GTCTGCACCTT GGGACAGGAA ATCCCGAGGA		
GAACGCCAAG ACTTCCAGAG GCTCATTGTT TTGCCCCGCT TTGCTTCGGA TTGAACCTCA		
CCGGCCGCAC AAGGATGCGT CCTGACACCT GGAGTCTCCG CTCACCCCTT CAGAGGCTCA		
CCAAGACAAA GGAACTAATT CCCATGGACT TTCCCTCCAGA GATGGAAATT GCTGGGATTT		
ACCCATCCCC TCCCCGTAC CCCCTTCCCC ACTAGGGAAA CAAGCTTGT TTAACCTTCT		
TATTCTTGG AGAAAGCACG GATGTCCCAG GTGCTGTCAA CAGCGCAGTC TTGACAATGG		
TCTATAGCAC AAAACAGTAC CATTACACCTG GCTGGATGAG CCGGCTGCC CAGAACGCTGC		
CTTCACTGTA CATATGTGAC TGCTCACATG TAACCAACAC AGGGACTTGT AGGGGGAAATC		
TCACTAATAC GAAATCCCAT TTTCAAGAGT CGCGGTGTCA ATAAACACTC TGTGGCTGGT		
GTCAAGGGTA ATCCCTTGAG CTTTCAGACA TTTCTGTTCC TGCCCCAGGAT TCGTTCCCTT		
GTTATCCATA TCCATCCCAG AACTGATGTT TTCTAAGGTA CTGAAACCCCC AAGTTGATGT		
GTGTCCCTGTG TTTAATGAC ATTGTATTTG TAAAGCAATT TTGTAGTATA AAAGTACCAT		
CTTCCAGTGT TCACATCCCC CCCAGCCAAT GACTAGCTCT TGGTATGAAA AAAAAAAATCT		
TTGAATTTTT GTAAAAAAAAA AAAAAAAAGTC GAC		
		1792

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Lys Asp Gly Gly Ser Phe Ser Gly Thr Gly Gly L u Pro Asp Tyr Ser
 1 5 10 15

Ala Pro Asn Pro Ile Lys Val Thr His Arg Cys Tyr Ile Leu Glu Asn
 20 25 30

Asp Thr Val Gln Cys Asp Leu Asp Leu Tyr Lys Ser Leu Gln Ala Trp
 35 40 45

Lys Asp His Lys Leu His Ile Asp His Glu Ile Glu Thr Leu Gln Asn
 50 55 60

Lys Ile Lys Asn Leu Arg Glu Val Arg Gly His Leu Lys Lys Lys Arg
 65 70 75 80

Pro Glu Glu Cys Asp Cys His Lys Val Ser Tyr His Ser Gln His Lys
 85 90 95

Gly Arg Leu Lys His Lys Gly Ser Ser Leu His Pro Phe Arg Lys Gly
 100 105 110

Leu Gln Glu Lys Asp Lys Val Trp Leu Leu Arg Glu Gln Lys Arg Lys
 115 120 125

Lys Lys Leu Arg Lys Leu Leu Lys Arg Leu Gln Asn Asn Asp Thr Cys
 130 135 140

Ser Met Pro Gly Leu Thr Cys Phe Thr His Asp Asn His His Trp Gln
 145 150 155 160

Thr Ala Pro Leu Trp Thr Leu Gly Pro Phe Cys Ala Cys Thr Ser Ala
 165 170 175

Asn Asn Asn Thr Tyr Trp Cys Leu Arg Thr Ile Asn Glu Thr His Asn
 180 185 190

Phe Leu Phe Cys Glu Phe Ala Thr Gly Phe Ile Glu Tyr Phe Asp Leu
 195 200 205

Ser Thr Asp Pro Tyr Gln Leu Met Asn Ala Val Asn Thr Leu Asp Arg
 210 215 220

Asp Val Leu Asn Gln Leu His Val Gln Leu Met Glu Leu Arg Ser Cys
 225 230 235 240

Lys Gly Tyr Lys Gln Cys Asn Pro Arg Thr Arg Asn Met Asp Leu Gly
 245 250 255

Leu Arg Asp Gly Gly Ser Tyr Glu Gln Tyr Arg Gln Phe Gln Arg Arg
 260 265 270

Lys Trp Pro Glu Met Lys Arg Pro Ser Ser Lys Ser Leu Gly Gln Leu
 275 280 285

Trp Glu Gly Trp Glu Gly
 290

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HW043

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 8..634

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 582..808
 (D) OTHER INFORMATION: /label= SAC_24533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTCGACG GCT CCA CCA GGT TCA AGA CAC AAA CCT GTG CCT ACC AAG TCA	49
Ala Pro Pro Gly Ser Arg His Lys Pro Val Pro Thr Lys Ser	
1 5 10	
ACA CCA GCT GGC ACA GAA CTA GGT AGC ACA GGA AGC GAC GGG GGA GAT	97
Thr Pro Ala Gly Thr Glu Leu Gly Ser Thr Gly Ser Asp Gly Gly Asp	
15 20 25 30	
GCA GTA GAA TAC AAC CCC AAC CTC CTG GAT GAC CCA CAG TGG CCG TGT	145
Ala Val Glu Tyr Asn Pro Asn Leu Leu Asp Asp Pro Gln Trp Pro Cys	
35 40 45	
GGG AAG CAC AAG CGT GTA CTC ATC TTT GCC TCA TAC ATG ACC ACT GTT	193
Gly Lys His Lys Arg Val Leu Ile Phe Ala Ser Tyr Met Thr Thr Val	
50 55 60	
ATA GAG TAT GTG AAG CCT GCA GAC CTC AAA AAG GAC ATG AAC GAG ACC	241
Ile Glu Tyr Val Lys Pro Ala Asp Leu Lys Asp Met Asn Glu Thr	
65 70 75	
TTC AGG GAG AAG TTC CCT CAT ATC AAA CTG ACA TTG AGC AAA ATT AGG	289
Phe Arg Glu Lys Phe Pro His Ile Lys Leu Thr Leu Ser Lys Ile Arg	
80 85 90	
AGT TTA AAA CGG GAG ATG CGG AAC CTT TCT GAA GAG TGC AGC TTG GAG	337
Ser Leu Lys Arg Glu Met Arg Asn Leu Ser Glu Glu Cys Ser Leu Glu	
95 100 105 110	
CCT GTG ACT GTG TCC ATG GCC TAT GTG TAC TTT GAG AAG CTT GCA CTG	385
Pro Val Thr Val Ser Met Ala Tyr Val Phe Glu Lys Leu Ala Leu	
115 120 125	
CAG GGC AAG CTC AAC AAA CAG AAC CGC AAA CTG TGT GCT GGC GCC TGT	433
Gln Gly Lys Leu Asn Lys Gln Asn Arg Lys Leu Cys Ala Gly Ala Cys	
130 135 140	

GTT CTG TTG GCT GCC AAG ATC AGC AGT GAC CTC CGC AAG AGT GAA GTG Val Leu Leu Ala Ala Lys Ile Ser Ser Asp Leu Arg Lys Ser Glu Val 145 150 155	481
AAG CAG CTT ATT GAC AAG CTG GAG GAA AGG TTC CGG TTC AAC AGG AAG Lys Gln Leu Ile Asp Lys Leu Glu Glu Arg Phe Arg Phe Asn Arg Lys 160 165 170	529
GAT CTC ATT GGA TTT GAG TTC ACG GTG CTT GTG GCT TTG GAA CTG GCC Asp Leu Ile Gly Phe Glu Phe Thr Val Leu Val Ala Leu Glu Leu Ala 175 180 185 190	577
CTG TAC CTC CCG GAG AAC CAA GTA TTA CCT CAC TAC AGA CGC CTC ACC Leu Tyr Leu Pro Glu Asn Gln Val Leu Pro His Tyr Arg Arg Leu Thr 195 200 205	625
CAG CAG TTC TAGCCCAGAA CAGTGCACCC CACAGGGAGC CTGCTTTGGC Gln Gln Phe	674
AGGAAGGCGA GTAGCTTGGC TAGAGCACTG ACTAGTAGTG TCCCTGTCCT TCCTCTAGTA ACTGCACTTG CCCCTCAGTC CAGGGCTGCA CTTAGCTTCC CTTGGAAAGA GGCAC TGCTC TTATTTTGGG GTGTACCCCCA TCTTCACCTT GAGGCCCTGT TGAGGGTTTT CCTGAAGCAA ATGAACATCG TGGGGCTTGG TTTGCTTTTC ATGTGCCTGA GACCAGCCTG GTTTATGTTG TCAATCCTGA GGTCCAGCTT TCATTTGCC TAGCCATGAA ACCATTCCCTG TAGAGACCTA GGTGTCCAGA CCTTCTGAAC ATACTGGAAT TGCCAGGCTT CTGCTCCTG GTGCCTCCAC CCAGGCAGAG CTCCCCCATC AGCACTTTT TTTGGTCAAG ATGCAGGAAA GGGCAGTCTG CTCACACTGG ACCTTGTAA AGCATCTGCC ACTGTGAAAC CCCTGTGCCA CCACATACAG TGTTTGGCCA ACACCACCA CCACCCCAAC CCCTGCCTCC TGCCAGCACT TATCCCTGCG GTACTGGACC ATTTAAGACA ACCGCTGACT GCAGGGCTCTT GACTTTCTG AGCAATATCA TGATGGAGAA AAGGTATTAA CTTGAGATTT GGTTTCTATA ACAGAAAAGA CGGGCCATTAA AGGCCTGCTG CTGACTCTGC ACCACACTTG ATCCTCAAGC AGGAAGGTAC TGACCCCTGCC ACCTAACAGC ACATCAGTGA CTCCTCACAA ATAGATGCCA TCCAGGCCA CTTGCCTGTG TATTGACTGT GCCACTGTCT TCCTACTGGC ACCAGACAAG AGCCATCCTC CACCTTCCCA GGCCTGTTAT TCCCTACAAC TGGTCACCAAG CCTGGCAGAT GCCAGTCCCA CTGCTCTCAA GTGCTGGTT CCACAGCCAC TCATCCCAGA AATGCTTACC CTCTCAAGCC TGACACCACT CAACTACCTA ATGGATGTTA GTAGCTAAA CAGAGACCTT GAAGGATAGT AGAAGGATAG TAAACTCTAG CCTTCTACCC TGCCCATGCT TATGCTGGTG TAAGCACGCT ATCCTTAGAG CACCTGGGTG CCATCTGCAG ACAGTGATGT CTTACTTAAA ATGAACTTA GATACAGCTG ACTGGTCGGC TATCCCTGGG GGTGATAACCC TGGTAGCTTA TTCTAGTTAT GTTAAAGCTG GCAACAGTGA TAATTTAACG TTCTATATTT ATGATCTTAC CAAGCTGGTG TGCTGTTAGT	734 794 854 914 974 1034 1094 1154 1214 1274 1334 1394 1454 1514 1574 1634 1694 1754 1814 1874 1934

CCTTCCTCC TTGCCCTCAG TAATGCTAAG AGCTGCTGAC ATGTGGTATG ATAAGCACTG	1994
TTACAACAAA ACCAACCTTT AAACCAAATG ACAGGCTAAA CACAGTGTCT GTCCTAGACT	2054
AAGTCCAGAA ATCCGAGGTG TGCCCACGGT GTCCAGCTGG ACTGTGACCC AATGCCACAG	2114
ACCTGGTGCT GTACCTTCAG CACTAACAG GCACAGCTGT GTGTGTGACC TCAGAATGCT	2174
GCTTATGTAT GTCCAGCCGG TTCTGAATGG AAGGTGTTAA ATGTTTTGT TAAAAGTAAA	2234
ACTTGTAAAAA GCAAAAAAAA AGTCGAC	2261

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Ala Pro Pro Gly Ser Arg His Lys Pro Val Pro Thr Lys Ser Thr Pro	
1 5 10 15	
Ala Gly Thr Glu Leu Gly Ser Thr Gly Ser Asp Gly Gly Asp Ala Val	
20 25 30	
Glu Tyr Asn Pro Asn Leu Leu Asp Asp Pro Gln Trp Pro Cys Gly Lys	
35 40 45	
His Lys Arg Val Leu Ile Phe Ala Ser Tyr Met Thr Thr Val Ile Glu	
50 55 60	
Tyr Val Lys Pro Ala Asp Leu Lys Asp Met Asn Glu Thr Phe Arg	
65 70 75 80	
Glu Lys Phe Pro His Ile Lys Leu Thr Leu Ser Lys Ile Arg Ser Leu	
85 90 95	
Lys Arg Glu Met Arg Asn Leu Ser Glu Glu Cys Ser Leu Glu Pro Val	
100 105 110	
Thr Val Ser Met Ala Tyr Val Tyr Phe Glu Lys Leu Ala Leu Gln Gly	
115 120 125	
Lys Leu Asn Lys Gln Asn Arg Lys Leu Cys Ala Gly Ala Cys Val Leu	
130 135 140	
Leu Ala Ala Lys Ile Ser Ser Asp Leu Arg Lys Ser Glu Val Lys Gln	
145 150 155 160	
Leu Ile Asp Lys Leu Glu Glu Arg Phe Arg Phe Asn Arg Lys Asp Leu	
165 170 175	
Ile Gly Phe Glu Phe Thr Val Leu Val Ala Leu Glu Leu Ala Leu Tyr	
180 185 190	
Leu Pro Glu Asn Gln Val Leu Pro His Tyr Arg Arg Leu Thr Gln Gln	
195 200 205	

Phe

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1538 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HW044

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 24..1100

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: complement (1161..1378)
 (D) OTHER INFORMATION: /label= SAC_24216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTGACCTCC ATAGAGTTCC GGC ATG AAG CCA CCG CAG AGA CGG CGG AAG	50
Met Lys Pro Pro Gln Arg Arg Arg Lys	
1 5	
GTC CCC GCA CGC TAC ACA GGT GAA GCT ACC GGC CCC ACA GCT TGG AGC	98
Val Pro Ala Arg Tyr Thr Gly Glu Ala Thr Gly Pro Thr Ala Trp Ser	
10 20 25	
CCC CGC GAG ATG CGG CAC CTA CTG AGA CTA CTC CAG GCT CGG CGC GGC	146
Pro Arg Glu Met Arg His Leu Leu Arg Leu Leu Gln Ala Arg Arg Gly	
30 35 40	
CAG CCG GAG CCA GAC GCC AAG GAG CTG GCC AAG GAG CTG CGA GGC CGG	194
Gln Pro Glu Pro Asp Ala Lys Glu Leu Ala Lys Glu Leu Arg Gly Arg	
45 50 55	
AGC GAG GCC GAG ATC TGT CGC TTT ATC CAG CAG CTC AAA GGC CGG GTG	242
Ser Glu Ala Glu Ile Cys Arg Phe Ile Gln Gln Leu Lys Gly Arg Val	
60 65 70	
GTT CGA GAG GCT ATT CGG AAG GTG CAA CCA GGT GGC AGA GAT GGT CCA	290
Val Arg Glu Ala Ile Arg Lys Val Gln Pro Gly Gly Arg Asp Gly Pro	
75 80 85	
AGG CAT CGA GAG ACA CAG CTC CCA GCC CCC ATA GAG GTA TGG ATG GAT	338
Arg His Arg Glu Thr Gln Leu Pro Ala Pro Ile Glu Val Trp Met Asp	
90 95 100 105	
CTT GCT GAG AAA TTA ACA GGC CCA CTG GAG GAA GCC CTG ACT GCA GCT	386
Leu Ala Glu Lys Leu Thr Gly Pro Leu Glu Glu Ala Leu Thr Ala Ala	
110 115 120	

TTC TCC CAG GTA CTC ACC ATT GCT GCG GAA CCT CTC AGC CTC CTG Phe Ser Gln Val Leu Thr Ile Ala Ala Ala Glu Pro Leu Ser Leu Leu 125 130 135	434
CAT TCC AAG CCA CGC AAG CCC ACA AAG GCC TGT GGA AGG GCA CTG GTG His Ser Lys Pro Gly Lys Pro Thr Lys Ala Cys Gly Arg Ala Leu Val 140 145 150	482
TTC TTG AGC ACC CAA GAT GCG CAG AAG GAT TCT GCC CCT GAA GGT TCT Phe Leu Ser Thr Gln Asp Ala Gln Lys Asp Ser Ala Pro Glu Gly Ser 155 160 165	530
GGG CCT GAA CCT ATG ACT GCT GCT GAC CCC ACT CCT GAG GCC TCT GTC Gly Pro Glu Pro Met Thr Ala Ala Asp Pro Thr Pro Glu Ala Ser Val 170 175 180 185	578
CCT GAA CCT AAG GCC TCC GGT ACC AAC CCT GAG ACC TCT GGC CTT GTC Pro Glu Pro Lys Ala Ser Gly Thr Asn Pro Glu Thr Ser Gly Leu Val 190 195 200	626
CCA GAG GTC TCT GTC CCT GAC CCT GAT GCA CCA ACT GAG TCC CTG GCT Pro Glu Val Ser Val Pro Asp Pro Asp Ala Pro Thr Glu Ser Leu Ala 205 210 215	674
GGA TCC TCC ACA GAG AGA GAC TTT GCC GTG GAC TTT GAG AAG ATC TAC Gly Ser Ser Thr Glu Arg Asp Phe Ala Val Asp Phe Glu Lys Ile Tyr 220 225 230	722
AAA TAC CTG TCC TCC TCC AGA GGT GGC CAT GGC CCT GAG CTC TCA Lys Tyr Leu Ser Ser Ser Arg Gly Gly His Gly Pro Glu Leu Ser 235 240 245	770
GCA GTT GAG TCC GCC GTG GTC CTT AAC CTG CTC ATG TCA CTT GCA GAG Ala Val Glu Ser Ala Val Val Leu Asn Leu Leu Met Ser Leu Ala Glu 250 255 260 265	818
GAA CTG CCC CAC CTG CCT TGC ACA GCC CTG GTG GAC CAT CTG ACT AAA Glu Leu Pro His Leu Pro Cys Thr Ala Leu Val Asp His Leu Thr Lys 270 275 280	866
ACA TAT GCT CAA CTG ACG GCT CCC CAG GCC TCT CTC GAT AGA GAA AAG Thr Tyr Ala Gln Leu Thr Ala Pro Gln Ala Ser Leu Asp Arg Glu Lys 285 290 295	914
AGG CCC AGG CCG GGG ACT GAA GAT GGA GGG ACT GAC TCC ACG GGG CCA Arg Pro Arg Pro Gly Thr Glu Asp Gly Gly Thr Asp Ser Thr Gly Pro 300 305 310	962
GAA GAG ACT GGC CAA GGC AGT CCT CAA GCT TCT GAG CCC ACA GAA CCG Glu Glu Thr Gly Gln Gly Ser Pro Gln Ala Ser Glu Pro Thr Glu Pro 315 320 325	1010
AGG CTG ACC TGG AAA GCA GCT GGG GTC TGC CCA CTG AAC CCA TTC CTG Arg Leu Thr Trp Lys Ala Ala Gly Val Cys Pro Leu Asn Pro Phe Leu 330 335 340 345	1058
G TG CCC CTG GAC CTC CTG AGC CAG GCC CTC CCT GCC AGG Val Pro Leu Asp Leu Leu Ser Gln Ala Leu Ala Pro Ala Arg 350 355	1100
TGAAGGATGC AGCAGGCTGG CTATGCTGGT TTCTTCTAC ATCGTCTGTC CAGCACTGGT	1160
ACTGGTGTGAG GGAAACGTGAT TGTGGCTTCC TGACAGTGTC CGGCCATAGG CAAGCCCTTC	1220

AGACACTGCA TGCAGTAGTA GCCTGGAAAG TGAAGCACAG TTGAAGGAAG GGGTTAAC	1280
ATTGGGGATT TGAGACTGCA CAAAGGCGGA ATTCCCTGGGC TGGTAGATTG CGGCAAGTGT	1340
CCCTGGCCCC GCTGTGCCG ATAAGAGTAC CACATCATCA TCCCTTG	1400
CATGGCACTC GAACCCACCC CCAGCACACC CTCCCCACCT CAACTGACCA CTGTACCATC	1460
CTCTTCGCCC TTCTCTGGGT GTCCCTGTGAC CCTCAATAAA GCTGTCATCT AACTAGCTGT	1520
GAAAAAAAAA AAGTCGAC	1538

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Lys Pro Pro Gln Arg Arg Arg Lys Val Pro Ala Arg Tyr Thr Gly	
1 5 10 15	
Glu Ala Thr Gly Pro Thr Ala Trp Ser Pro Arg Glu Met Arg His Leu	
20 25 30	
Leu Arg Leu Leu Gln Ala Arg Arg Gly Gln Pro Glu Pro Asp Ala Lys	
35 40 45	
Glu Leu Ala Lys Glu Leu Arg Gly Arg Ser Glu Ala Glu Ile Cys Arg	
50 55 60	
Phe Ile Gln Gln Leu Lys Gly Arg Val Val Arg Glu Ala Ile Arg Lys	
65 70 75 80	
Val Gln Pro Gly Gly Arg Asp Gly Pro Arg His Arg Glu Thr Gln Leu	
85 90 95	
Pro Ala Pro Ile Glu Val Trp Met Asp Leu Ala Glu Lys Leu Thr Gly	
100 105 110	
Pro Leu Glu Glu Ala Leu Thr Ala Ala Phe Ser Gln Val Leu Thr Ile	
115 120 125	
Ala Ala Ala Glu Pro Leu Ser Leu Leu His Ser Lys Pro Gly Lys Pro	
130 135 140	
Thr Lys Ala Cys Gly Arg Ala Leu Val Phe Leu Ser Thr Gln Asp Ala	
145 150 155 160	
Gln Lys Asp Ser Ala Pro Glu Gly Ser Gly Pro Glu Pro Met Thr Ala	
165 170 175	
Ala Asp Pro Thr Pro Glu Ala Ser Val Pro Glu Pro Lys Ala Ser Gly	
180 185 190	
Thr Asn Pro Glu Thr Ser Gly Leu Val Pro Glu Val Ser Val Pro Asp	
195 200 205	

Pro Asp Ala Pro Thr Glu Ser Leu Ala Gly Ser Ser Thr Glu Arg Asp
 210 215 220
 Phe Ala Val Asp Phe Glu Lys Ile Tyr Lys Tyr Leu Ser Ser Ser Ser
 225 230 235 240
 Arg Gly Gly His Gly Pro Glu Leu Ser Ala Val Glu Ser Ala Val Val
 245 250 255
 Leu Asn Leu Leu Met Ser Leu Ala Glu Glu Leu Pro His Leu Pro Cys
 260 265 270
 Thr Ala Leu Val Asp His Leu Thr Lys Thr Tyr Ala Gln Leu Thr Ala
 275 280 285
 Pro Gln Ala Ser Leu Asp Arg Glu Lys Arg Pro Arg Pro Gly Thr Glu
 290 295 300
 Asp Gly Gly Thr Asp Ser Thr Gly Pro Glu Glu Thr Gly Gln Gly Ser
 305 310 315 320
 Pro Gln Ala Ser Glu Pro Thr Glu Pro Arg Leu Thr Trp Lys Ala Ala
 325 330 335
 Gly Val Cys Pro Leu Asn Pro Phe Leu Val Pro Leu Asp Leu Leu Ser
 340 345 350
 Gln Ala Leu Ala Pro Ala Arg
 355

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2277 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: HW045

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 9..1628

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1973..2134
 - (D) OTHER INFORMATION: /label= SAC_24028

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GTCGGACCA GGG CGT GAT GGC TCC TAC TAC CAG CTC TTT GTT CAT GGT GGC
 Gly Arg Asp Gly Ser Tyr Tyr Gln Leu Phe Val His Gly Gly
 1 5 10

50

CGC CTC CAG CCA GTC CTA AGG CAG AAA GCC TGC CGA GGC ATG AAC TGG Arg Leu Gln Pro Val Leu Arg Gln Lys Ala Cys Arg Gly Met Asn Trp 15 20 25 30	98
ATA GCT GGG CTT CGG ATG GTG CCC GAT GGC AGT ATG GTC GTC TTG GGT Ile Ala Gly Leu Arg Met Val Pro Asp Gly Ser Met Val Val Leu Gly 35 40 45	146
TTC CAT GCC AAC GAG TTT GTA GTG TGG AGC CCG CGG TCC CAT GAG AAG Phe His Ala Asn Glu Phe Val Val Trp Ser Pro Arg Ser His Glu Lys 50 55 60	194
CTG CAC ATC GTC AAC TGC GGG GGA GGG CAC CGC TCC TGG GCC TTT TCT Leu His Ile Val Asn Cys Gly Gly His Arg Ser Trp Ala Phe Ser 65 70 75	242
GAT ACT GAG GCA GCC ATG GCC TTT GCC TAC CTT AAG GAT GGT GAT GTC Asp Thr Glu Ala Ala Met Ala Phe Ala Tyr Leu Lys Asp Gly Asp Val 80 85 90	290
ATG CTC TAC CCG GCT CTA GGA GGC TGC ATC AGG CCA AAC GTG ATT CTC Met Leu Tyr Arg Ala Leu Gly Gly Cys Ile Arg Pro Asn Val Ile Leu 95 100 105 110	338
CGG GAG GGT CTG CAT GGC CGG GAA ATC ACA TGT GTA AAG CGT GTG GGC Arg Glu Gly Leu His Gly Arg Glu Ile Thr Cys Val Lys Arg Val Gly 115 120 125	386
ACT GTT ACC CTG GGC CCT GAA TTT GAG GTA CCC AAC TTG GAG CAT CCT Thr Val Thr Leu Gly Pro Glu Phe Glu Val Pro Asn Leu Glu His Pro 130 135 140	434
GAC TCC CTG GAG CCT GGC AGT GAG GGG CCT GGT CTG ATT GAC ATC GTG Asp Ser Leu Glu Pro Gly Ser Glu Gly Pro Gly Leu Ile Asp Ile Val 145 150 155	482
ATA ACA GGC AGT GAG GAC ACT ACT GTC TGT GTG CTA GCA CTT CCC ACC Ile Thr Gly Ser Glu Asp Thr Thr Val Cys Val Leu Ala Leu Pro Thr 160 165 170	530
ACC ACA GGC GCA GCC CAC GCC CTC ACT GCT GTC TGT AAC CAT ATC TCC Thr Thr Gly Ala Ala His Ala Leu Thr Ala Val Cys Asn His Ile Ser 175 180 185 190	578
TCC GTG CGA GCC CTG GCA GTG TGG GGT GTT GGC ACC CCA GGT GGC CCA Ser Val Arg Ala Leu Ala Val Trp Gly Val Gly Thr Pro Gly Gly Pro 195 200 205	626
CAG GAT TCT CAC CCA GGG CTC ACG GCT CAG GTA GTG TCT GCA GGG GGT Gln Asp Ser His Pro Gly Leu Thr Ala Gln Val Val Ser Ala Gly Gly 210 215 220	674
CGA GCC GAG ATG CAC TGC TTC AGC CTC ATG ATC ACT CCG GAT GCC AGC Arg Ala Glu Met His Cys Phe Ser Leu Met Ile Thr Pro Asp Ala Ser 225 230 235	722
ACC CCA AGC CGC CTT GCC TGC CAC ATC ATG CAC CTT TCA TCC CAC CGG Thr Pro Ser Arg Leu Ala Cys His Ile Met His Leu Ser Ser His Arg 240 245 250	770
CTA GAT GAG TAC TGG GAC CGG CAG CGC AAC CGG CAC CGG ATG ATC AAG Leu Asp Glu Tyr Trp Asp Arg Gln Arg Asn Arg His Arg Met Ile Lys 255 260 265 270	818

G TG GAC CCT GAG ACC AGG TAC ATG TCT CTT GCC ATT TGT GAG CTT GAC Val Asp Pro Glu Thr Arg Tyr Met Ser Leu Ala Ile Cys Glu Leu Asp 275 280 285	866
T CC GAT AGG CCT GGC CTT GGC CCC GGC CCC CTT GTG GCT GCA GCC TGT Ser Asp Arg Pro Gly Leu Gly Pro Gly Pro Leu Val Ala Ala Cys 290 295 300	914
A GT GAC GGG GCA GTG AGG CTT TTT CTC TTG CAG GAC TCT GGG CGA ATT Ser Asp Gly Ala Val Arg Leu Phe Leu Leu Gln Asp Ser Gly Arg Ile 305 310 315	962
C TG CAT CTC CTT GCT GAG ACT TTC CAC CAT AAG CGG TGT GTC CTC AAG Leu His Leu Ala Glu Thr Phe His His Lys Arg Cys Val Leu Lys 320 325 330	1010
G TC CAT TCG TTC ACA CAT GAG GCA CCC AAC CAG CGT CGG AGG CTG ATC Val His Ser Phe Thr His Glu Ala Pro Asn Gln Arg Arg Arg Leu Ile 335 340 345 350	1058
C TG TGC AGT GCA GCT ACA GAT GGC AGC ATA GCC TTC TGG GAT CTC ACC Leu Cys Ser Ala Ala Thr Asp Gly Ser Ile Ala Phe Trp Asp Leu Thr 355 360 365	1106
A CG GCA ATG GAC CGA GGC TCT ACT ACC CTG GAG CCT CCA GCA CAC CCT Thr Ala Met Asp Arg Gly Ser Thr Thr Leu Glu Pro Pro Ala His Pro 370 375 380	1154
G GG CTT CCC TAC CAG ATG GGC ACC CCC TGC CTG ACC GTC CAG GCC CAT Gly Leu Pro Tyr Gln Met Gly Thr Pro Cys Leu Thr Val Gln Ala His 385 390 395	1202
A GC TGT GGT GTC AAC AGC CTG CAC ACT TTG CCT ACA CCT GAG GGC CAT Ser Cys Gly Val Asn Ser Leu His Thr Leu Pro Thr Pro Glu Gly His 400 405 410	1250
C AT CTT GTG GCC AGT GGC AGT GAG GAC GGG TCC CTG CAT GTC TTC ACG His Leu Val Ala Ser Gly Ser Glu Asp Gly Ser Leu His Val Phe Thr 415 420 425 430	1298
C TT GCT GTG AAG ATG CCA GAG CTG GAA GAG GCT GAT GGG GAG GCT GAG Leu Ala Val Lys Met Pro Glu Leu Glu Ala Asp Gly Glu Ala Glu 435 440 445	1346
T TG GTG CCC CAG TTA TGT GTC CTA GAT GAA TAT TCT GTC CCC TGT GCA Leu Val Pro Gln Leu Cys Val Leu Asp Glu Tyr Ser Val Pro Cys Ala 450 455 460	1394
C AT GCT GCC CAT GTG ACG GGC ATC AAG ATC CTA AGT CCC AAG CTG ATG His Ala Ala His Val Thr Gly Ile Lys Ile Leu Ser Pro Lys Leu Met 465 470 475	1442
G TC TCA GCC TCC ATA GAC CAA CGG CTG ACC TTC TGG CGT CTT GGA AAT Val Ser Ala Ser Ile Asp Gln Arg Leu Thr Phe Trp Arg Leu Gly Asn 480 485 490	1490
G GT GAG CCC ACC TTC ATG AAT AGC ACT GTG TAC CAC GTG CCA GAT GTG Gly Glu Pro Thr Phe Met Asn Ser Thr Val Tyr His Val Pro Asp Val 495 500 505 510	1538
G CT GAC ATG GAC TGC TGG CCT GTG AAC CCT GAG TTT GGC CAC CGC TGT Ala Asp Met Asp Cys Trp Pro Val Asn Pro Glu Phe Gly His Arg Cys	1586

515	520	525	
GCT CTT GCG GGT CAG GGA CTC GAG GTT TAC AAC TGG TAT GAC Ala Leu Ala Gly Gln Gly Leu Glu Val Tyr Asn Trp Tyr Asp 530 535 540			1628
TGAGTTACCA CAGTAGTTGG AGGACTGAGC CTGGGGCTTG ACCACAGACA GCGGAGCAGG			1688
GATCAGCTGT CTGTGTCTAG CTCTATGTGC TCTGAGGAGG TGAGGCAGTA CCATGGGTTTC			1748
CTGTAGGGTG TTGCATAGGT GGACCAAGAA TATGCCTCAC TCTTCACAAT AGGATGAAAC			1808
TGTATTTATT CTGACTTTAA GTGCCAACA TCTGTGAGGT TTCTGTGAGG TCTTGTTTT			1868
TTCCCAAGTTG ATGCTTTTAT AAACATTCCC AGCTATTGGG CCCTTAGATG TGGCTCAGCG			1928
GAGGGAGGCC CAGCATGGCC AAGCCTGTGT GGAACACCTC ACGTACTGCC CTCAAAAGCT			1988
GTAGGCGAGC AAACATCTGA CCAAAGAGGT GTGGCCGAGG TTCCCTGAAAG AAAAGCAACC			2048
AGGCCCATCC TCATTTCCCG AGCCTGAGCC CTTGTCCATA TTTCCCACAG ACCCTCCCTT			2108
GCTGTATGCT CACCCCTAGA ATGTGTACGC GGTTATAGTA TGAGCTGAAA TCCATGCTGA			2168
GCTGCACCAG GAACTTGCAC ACCTAGAGAC AGAGGTTGGA TCGTTGAGCT GTTGTCTTT			2228
TTCTTGTC ACAACCCAGA ATAAAGAATA GTGTGTGTAG TGTCAAAAA			2277

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly Arg Asp Gly Ser Tyr Tyr Gln Leu Phe Val His Gly Gly Arg Leu			
1 5 10 15			
Gln Pro Val Leu Arg Gln Lys Ala Cys Arg Gly Met Asn Trp Ile Ala			
20 25 30			
Gly Leu Arg Met Val Pro Asp Gly Ser Met Val Val Leu Gly Phe His			
35 40 45			
Ala Asn Glu Phe Val Val Trp Ser Pro Arg Ser His Glu Lys Leu His			
50 55 60			
Ile Val Asn Cys Gly Gly His Arg Ser Trp Ala Phe Ser Asp Thr			
65 70 75 80			
Glu Ala Ala Met Ala Phe Ala Tyr Leu Lys Asp Gly Asp Val Met Leu			
85 90 95			
Tyr Arg Ala Leu Gly Gly Cys Ile Arg Pro Asn Val Ile Leu Arg Glu			
100 105 110			
Gly Leu His Gly Arg Glu Ile Thr Cys Val Lys Arg Val Gly Thr Val			
115 120 125			

Thr Leu Gly Pro Glu Phe Glu Val Pro Asn Leu Glu His Pro Asp Ser
130 135 140

Leu Glu Pro Gly Ser Glu Gly Pro Gly Leu Ile Asp Ile Val Ile Thr
145 150 155 160

Gly Ser Glu Asp Thr Thr Val Cys Val Leu Ala Leu Pro Thr Thr Thr
165 170 175

Gly Ala Ala His Ala Leu Thr Ala Val Cys Asn His Ile Ser Ser Val
180 185 190

Arg Ala Leu Ala Val Trp Gly Val Gly Thr Pro Gly Gly Pro Gln Asp
195 200 205

Ser His Pro Gly Leu Thr Ala Gln Val Val Ser Ala Gly Gly Arg Ala
210 215 220

Glu Met His Cys Phe Ser Leu Met Ile Thr Pro Asp Ala Ser Thr Pro
225 230 235 240

Ser Arg Leu Ala Cys His Ile Met His Leu Ser Ser His Arg Leu Asp
245 250 255

Glu Tyr Trp Asp Arg Gln Arg Asn Arg His Arg Met Ile Lys Val Asp
260 265 270

Pro Glu Thr Arg Tyr Met Ser Leu Ala Ile Cys Glu Leu Asp Ser Asp
275 280 285

Arg Pro Gly Leu Gly Pro Gly Pro Leu Val Ala Ala Ala Cys Ser Asp
290 295 300

Gly Ala Val Arg Leu Phe Leu Leu Gln Asp Ser Gly Arg Ile Leu His
305 310 315 320

Leu Leu Ala Glu Thr Phe His His Lys Arg Cys Val Leu Lys Val His
325 330 335

Ser Phe Thr His Glu Ala Pro Asn Gln Arg Arg Arg Leu Ile Leu Cys
340 345 350

Ser Ala Ala Thr Asp Gly Ser Ile Ala Phe Trp Asp Leu Thr Thr Ala
355 360 365

Met Asp Arg Gly Ser Thr Thr Leu Glu Pro Pro Ala His Pro Gly Leu
370 375 380

Pro Tyr Gln Met Gly Thr Pro Cys Leu Thr Val Gln Ala His Ser Cys
385 390 395 400

Gly Val Asn Ser Leu His Thr Leu Pro Thr Pro Glu Gly His His Leu
405 410 415

Val Ala Ser Gly Ser Glu Asp Gly Ser Leu His Val Phe Thr Leu Ala
420 425 430

Val Lys Met Pro Glu Leu Glu Ala Asp Gly Glu Ala Glu Leu Val
435 440 445

Pro Gln Leu Cys Val Leu Asp Glu Tyr Ser Val Pro Cys Ala His Ala
450 455 460

Ala His Val Thr Gly Ile Lys Ile Leu Ser Pro Lys Leu Met Val S r
 465 470 475 480

Ala Ser Ile Asp Gln Arg Leu Thr Phe Trp Arg Leu Gly Asn Gly Glu
 485 490 495

Pro Thr Phe Met Asn Ser Thr Val Tyr His Val Pro Asp Val Ala Asp
 500 505 510

Met Asp Cys Trp Pro Val Asn Pro Glu Phe Gly His Arg Cys Ala Leu
 515 520 525

Ala Gly Gln Gly Leu Glu Val Tyr Asn Trp Tyr Asp
 530 535 540

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HW046

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 9..1160

(xi) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: complement (1523..1760)
- (D) OTHER INFORMATION: /label= SAC_24036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTGCGACGT GAC TTC CTT GTC AGG TTC ACC CCC GCT GCA GCA GGG CTC TGC	50
Asp Phe Leu Val Arg Phe Thr Pro Ala Ala Gly Leu Cys	
1 5 10	

TCT CTG ACT GAG TGG TGC TGT GTT ACA TGG ATC TGT CAT TTC TAT TCA	98
Ser Leu Thr Glu Trp Cys Cys Val Thr Trp Ile Cys His Phe Tyr Ser	
15 20 25 30	

GTC ATC AGT TGG CAT TGC AGT AAC ACC TAT GGC AAT GAA GAA AGA GAC	146
Val Ile Ser Trp His Cys Ser Asn Thr Tyr Gly Asn Glu Glu Arg Asp	
35 40 45	

AGA ATT TGG GAT TTT CAT CTA AGG AAA ATG ATA AAT AAC AAC CAG ACG	194
Arg Ile Trp Asp Phe His Leu Arg Lys Met Ile Asn Asn Asn Gln Thr	
50 55 60	

TGT GCT GCA GGG CAG GAC TCC GTG CCC TAC GTG ACC TGT ATG CTT CAC	242
Cys Ala Ala Gly Gln Asp Ser Val Pro Tyr Val Thr Cys Met Leu His	
65 70 75	

GTG CTG GAA GAG TGG TTG GGT GTG GAA CAG TTG GAG GAC TAC CTG AAT Val Leu Glu Glu Trp Leu Gly Val Glu Gln Leu Glu Asp Tyr Leu Asn 80 85 90	290
TTT GCG AAC CAT CTC TTG TGG GTC TTC ACC CCG CTG ATC CTT TTA ATA Phe Ala Asn His Leu Leu Trp Val Phe Thr Pro Leu Ile Leu Leu Ile 95 100 105 110	338
CTT CCG TAC TTT ACC ATC TTC CTT CTC TAC CTT ACT ATT ATT TTC CTC Leu Pro Tyr Phe Thr Ile Phe Leu Leu Tyr Leu Thr Ile Ile Phe Leu 115 120 125	386
CAC ATC TAT AAG AGG AAG AAT GTG TTA AAA GAA GCC TAC TCT CAC AAC His Ile Tyr Lys Arg Lys Asn Val Leu Lys Glu Ala Tyr Ser His Asn 130 135 140	434
TTG TGG GAT GGC GCG AGG AAA ACA GTG GCA ACC CTG TGG GAT GGA CAT Leu Trp Asp Gly Ala Arg Lys Thr Val Ala Thr Leu Trp Asp Gly His 145 150 155	482
GCG GCG GTT TGG CAT GGT TAT GAA GTT CAC GGG ATG GAA AAG ATA CCA Ala Ala Val Trp His Gly Tyr Glu Val His Gly Met Glu Lys Ile Pro 160 165 170	530
GAA GGA CCA GCA CTT ATA ATT TTT TAT CAT GGA GCT ATT CCC ATA GAC Glu Gly Pro Ala Leu Ile Ile Phe Tyr His Gly Ala Ile Pro Ile Asp 175 180 185 190	578
TTT TAC TAC TTC ATG GCT AAA ATT TTC ATC CAC AAA GGC AGA ACT TGC Phe Tyr Tyr Phe Met Ala Lys Ile Phe Ile His Lys Gly Arg Thr Cys 195 200 205	626
CGA GTG GTA GCT GAC CAC TTT GTC TTT AAA ATC CCA GGG TTC AGT TTA Arg Val Val Ala Asp His Phe Val Phe Lys Ile Pro Gly Phe Ser Leu 210 215 220	674
TTA CTT GAT GTA TTT TGT GCT CTT CAT GGA CCA AGA GAA AAA TGT GTT Leu Leu Asp Val Phe Cys Ala Leu His Gly Pro Arg Glu Lys Cys Val 225 230 235	722
GAA ATC TTG AGG AGT GGT CAC TTG TTA GCT ATT TCA CCG GGT GGA GTT Glu Ile Leu Arg Ser Gly His Leu Leu Ala Ile Ser Pro Gly Gly Val 240 245 250	770
CGA GAA GCC TTA CTT AGT GAT GAA ACC TAC AAC ATC ATA TGG GGT AAT Arg Glu Ala Leu Leu Ser Asp Glu Thr Tyr Asn Ile Ile Trp Gly Asn 255 260 265 270	818
CGT AAA GGC TTT GCT CAG GTT GCA ATC GAT GCA AAA GTG CCC ATT ATT Arg Lys Gly Phe Ala Gln Val Ala Ile Asp Ala Lys Val Pro Ile Ile 275 280 285	866
CCT ATG TTT ACA CAA AAC ATC CGA GAA GGA TTT AGA TCA CTC GGA GGA Pro Met Phe Thr Gln Asn Ile Arg Glu Gly Phe Arg Ser Leu Gly Gly 290 295 300	914
ACA AGA TTG TTT AAA TGG CTT TAT GAA AAA TTC CGC TAT CCG TTT GCT Thr Arg Leu Phe Lys Trp Leu Tyr Glu Lys Phe Arg Tyr Pro Phe Ala 305 310 315	962
CCA ATG TAT GGA GGT TTT CCT GTG AAG TTG CGG ACC TTC TTG GGT GAT Pro Met Tyr Gly Phe Pro Val Lys Leu Arg Thr Phe Leu Gly Asp	1010

320	325	330	
CCT ATT CCG TAT GAC CCA GAG GTA ACA GCA GAA GAA TTA GCT GAA AAG Pro Ile Pro Tyr Asp Pro Glu Val Thr Ala Glu Glu Leu Ala Glu Lys 335 340 345 350			1058
ACT AAG AAC GCT GTT CAA GCT TTG ATC GAC AAG CAC CAA AGG ATA CCG Thr Lys Asn Ala Val Gln Ala Leu Ile Asp Lys His Gln Arg Ile Pro 355 360 365			1106
GGG AAC ATT AGG AGT GCT TTG CTG GAC CGC TTT CAT AAA GAG CAG AAG Gly Asn Ile Arg Ser Ala Leu Leu Asp Arg Phe His Lys Glu Gln Lys 370 375 380			1154
GCT AAT TGACAGATAA TTTCGTGTGT CTCTAATGCC AAGTTGCAT CTGTGGTACT Ala Asn			1210
GCCTTTAAA CTTTTGAGG TTGTATAATA GTCTTTAA AACCTGCTAA TGAGCATCTT TCTTTAGAAT TTAAACTTTC TATGGTTAAT CTTACCCCTT CAATCAGTTT TGTCAAATGT AGTAAGTAAC TCACCATTG CTTGACTCAG AAGATGATCA TGTGCAATT GCAATCCTTA GTAGTATATG ATAGGCACAA GTCTTCCCTGG ATAACAGCAG TCTAGGTTAG GCAGACTTCA CTAAATTATG CTTCTGTGTT TGTGTCTGTT GTGCCAATGG GATGGTGAGA GGTACCTGAG CTGGGGTGTGTA GCACCTGCTT AGTTTAGGTG AGCGGTGCCT TTGATCCAT CCTTCATTCC ACTCACAAC TGTGGTAAGT TGTGGAACGC TTTTGACCT CCGTGGTTA TGTAAAGCAT GGTAATACTG TGGTGGTGAA CATTAAAGTTG CTTATGTCTA CTGTGATATA TCCGTATCTA TATATCTGAT AGATATCTGT AGTGAGAAAT CTGTAATTGA ATTGATTCCCT GAATCCTTA GGAGTTATGT ACATTTTTGT CCATTGGTA TTGAAATTAC TCCTTCAGGG ATGATGTCCA GTTGCCAAGC ACAATGAAAG AGATGACTA TTTTGTAAAT CAAATCATTG TTACTTGTAG TATTTATTAA CAGAGTTGTT TGGTATTTAT TTTAAACAAG GATCTAAGTA AATGTATAGG ATGGATTGTC AGCACGTGTC TTACACGGTG TAAAGATAAA ATCGTGGGCA CGCTCTGCAG TTTATGTTAG AGCAGATCCT AGGCTGAGGA GTGACAACCTG AGGAAGCTCT GCCTCGCTTA TCCCAGGGCT CGCTTCCGTG CTCTGCAGCC AGTCACGTGG TTATATCTGT AAAATGTACT TGAATGATGA ATTCTGTAA ACATGGAGTC CTCTGAAAT GTAATTACTT TGAATTGTTG TCTTCTGAA AACATTATTT AAAAGTATT AAACAGCCAA GTATCATGAA TTCATCGCAG TGTGTCTTCC CCCTTGCAG TACTTGGGTT TTATATGGAC TTTTTAACTA CAAGTGTATA TTTGTGATAT GTATAATGTA TGTATAATGT ATATAGAAAT GGTGTGAAAA TAAAGCTGAA CTGCAACTCC TCTCTAGTAA AAA		1270 1330 1390 1450 1510 1570 1630 1690 1750 1810 1870 1930 1990 2050 2110 2170 2230 2290 2350 2373	

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 384 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Asp Phe Leu Val Arg Phe Thr Pro Ala Ala Ala Gly Leu Cys Ser Leu
1 5 10 15

Thr Glu Trp Cys Cys Val Thr Trp Ile Cys His Phe Tyr Ser Val Ile
20 25 30

Ser Trp His Cys Ser Asn Thr Tyr Gly Asn Glu Glu Arg Asp Arg Ile
35 40 45

Trp Asp Phe His Leu Arg Lys Met Ile Asn Asn Asn Gln Thr Cys Ala
50 55 60

Ala Gly Gln Asp Ser Val Pro Tyr Val Thr Cys Met Leu His Val Leu
65 70 75 80

Glu Glu Trp Leu Gly Val Glu Gln Leu Glu Asp Tyr Leu Asn Phe Ala
85 90 95

Asn His Leu Leu Trp Val Phe Thr Pro Leu Ile Leu Leu Ile Leu Pro
100 105 110

Tyr Phe Thr Ile Phe Leu Leu Tyr Leu Thr Ile Ile Phe Leu His Ile
115 120 125

Tyr Lys Arg Lys Asn Val Leu Lys Glu Ala Tyr Ser His Asn Leu Trp
130 135 140

Asp Gly Ala Arg Lys Thr Val Ala Thr Leu Trp Asp Gly His Ala Ala
145 150 155 160

Val Trp His Gly Tyr Glu Val His Gly Met Glu Lys Ile Pro Glu Gly
165 170 175

Pro Ala Leu Ile Ile Phe Tyr His Gly Ala Ile Pro Ile Asp Phe Tyr
180 185 190

Tyr Phe Met Ala Lys Ile Phe Ile His Lys Gly Arg Thr Cys Arg Val
195 200 205

Val Ala Asp His Phe Val Phe Lys Ile Pro Gly Phe Ser Leu Leu Leu
210 215 220

Asp Val Phe Cys Ala Leu His Gly Pro Arg Glu Lys Cys Val Glu Ile
225 230 235 240

Leu Arg Ser Gly His Leu Leu Ala Ile Ser Pro Gly Gly Val Arg Glu
245 250 255

Ala Leu Leu Ser Asp Glu Thr Tyr Asn Ile Ile Trp Gly Asn Arg Lys
260 265 270

Gly Phe Ala Gln Val Ala Ile Asp Ala Lys Val Pro Ile Ile Pro Met
275 280 285

Phe Thr Gln Asn Ile Arg Glu Gly Phe Arg Ser Leu Gly Gly Thr Arg
290 295 300

Leu Phe Lys Trp Leu Tyr Glu Lys Phe Arg Tyr Pro Phe Ala Pro Met
 305 310 315 320
 Tyr Gly Gly Phe Pro Val Lys Leu Arg Thr Phe Leu Gly Asp Pro Ile
 325 330 335
 Pro Tyr Asp Pro Glu Val Thr Ala Glu Glu Leu Ala Glu Lys Thr Lys
 340 345 350
 Asn Ala Val Gln Ala Leu Ile Asp Lys His Gln Arg Ile Pro Gly Asn
 355 360 365
 Ile Arg Ser Ala Leu Leu Asp Arg His Phe Lys Glu Gln Lys Ala Asn
 370 375 380

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HW047

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 8..511

(xi) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: complement (1675..1833)
 (D) OTHER INFORMATION: /label= SAC_23915

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GTCGACC AGG GCC TTC CAT CAG ACC TGC CCA AAC TTT GTC ATA GAG AAG	49
Arg Ala Phe His Gln Thr Cys Pro Asn Phe Val Ile Glu Lys	
1 5 10	
ATT GAA AGG ATT CAA AAT CCA GCT CTT TGG AGG AGG TAC CAG GCG TAC	97
Ile Glu Arg Ile Gln Asn Pro Ala Leu Trp Arg Arg Tyr Gln Ala Tyr	
15 20 25 30	
AAA AAA ATT ATG GAT GAA AAG AAT GGC AAT GTG ATA AAT GAG AAG CAA	145
Lys Lys Ile Met Asp Glu Lys Asn Gly Asn Val Ile Asn Glu Lys Gln	
35 40 45	
CTC TTC CAT GGG ACG GAG TTT GGC TCT CTG GCA CAG CTC AAC AGT AAT	193
Leu Phe His Gly Thr Glu Phe Gly Ser Leu Ala Gln Leu Asn Ser Asn	
50 55 60	
GGA TTT AAC CGC AGC TAT GCT GGG AAG AAC GCT ACG GCT TAT GGG AAA	241
Gly Phe Asn Arg Ser Tyr Ala Gly Lys Asn Ala Thr Ala Tyr Gly Lys	

65	70	75	
GGA ACC TAT TTT GCA GTC AAT GCT TCC TAT TCT GCC CAT GAC ACA TAT Gly Thr Tyr Phe Ala Val Asn Ala Ser Tyr Ser Ala His Asp Thr Tyr			289
80	85	90	
TCC AAA CCA GAT GCC AAT GGG AAA AAG TAT ATG TAT TAT GTG CGG GTC Ser Lys Pro Asp Ala Asn Gly Lys Tyr Met Tyr Tyr Val Arg Val			337
95	100	105	110
CTC ACT GGA AAC TAC ACA CAA GGA AAC GCA TCA CTG ATT GTG CCT CCT Leu Thr Gly Asn Tyr Thr Gln Gly Asn Ala Ser Leu Ile Val Pro Pro			385
115	120	125	
TCA AGG GAC CCT CAA AAT GCT ACT GAC TTG TTT GAC ACT GTC GCA GAT Ser Arg Asp Pro Gln Asn Ala Thr Asp Leu Phe Asp Thr Val Ala Asp			433
130	135	140	
AAT GTT ATA AAT CCG AGT ATA TTT GTA GTG TTT TAT GAC AAT CAA GCA Asn Val Ile Asn Pro Ser Ile Phe Val Val Phe Tyr Asp Asn Gln Ala			481
145	150	155	
TAC CCT GAG TAT CTT ATC ACA TTT AGG AAG TAACACTTG GGGTGCCTTC Tyr Pro Glu Tyr Leu Ile Thr Phe Arg Lys			531
160	165		
TGAAAGACAT TGGTATCTGC CGTAGGACAA ATTTAGCTG TTTCTCTCT TAGACTTCT			591
TCTCTAACAG CACGAGGTCT TTCTCTGCCA CGGATTGTTT CCTCAGCTGC CCCTTCATAG			651
TGAACATGAA CCTACTTGAG GGCCAACCAC TTGAGAATT CAAGCAGGTG ACAGCTTAG			711
CTGCCTTCAC AAATGTGAAC CTCAAATCCA CGGAAAAGAA CAAACTTACG TTCTGGAAGG			771
ACAATAAAC CTTTATGCAC TTTCAGAAAG CCCACAATAC ACCCACCACC AGTGGAGTTA			831
CATCAGAGCA CCACTGTGCT GAGGGCACC CAGGACCACT GAGCCAGTAA GGCTGCCAAC			891
TGAACAGATT CCAAGACAGA GAACTTCGTT CATCACTAAC AGCGCCGTGT CCTGTGGTT			951
GGACAGTTCC AGCCAGGGTT ATGTACAGAC TGGGTTCTGG GATGTGGCTC TGGGTCTGTG			1011
TGAACTGAGC CCCCCAAGGA GAGGCACAGC TGAAGCCCTG TCAGGGGGCC CTTTTAATGT			1071
TGACACCAAT GTTGAGGCTA CCTAGTGAAG AAATGGGATG GGGCCTGCTA CCTCTCCTGT			1131
GGAAAGTCCTT CTACTGGGTG AAAATGAATG AACTCTAACAA GTATTGGCTA GCGTCTTCT			1191
TGTGGCAGGC TGGCTTGTGA TAACTTGAG CTTTATGACT AAGTCAGTCA TTTTGCTAAC			1251
TCACTAACAG TATCTACTGG ATGCGATTTG TTTCTTGTGA TGCCAGAGAT CACCCAGAGC			1311
CTCACATGGG CCAGGCAAGC ACTCTACTAC TGAACATATAT TCCCAGCCTC TTAGTGAGGC			1371
AAGACTCCAC TAAGTTGCCG TGGCAGGTTT GAACTCATTA TCTTCCTGCA TTGGCTACTT			1431
ATTGGGGTGG GGTGGGGTGC TTAAATTGTT CTTTTAATTT TCTCTGTAC TCCCATTAT			1491
TGAGTGCCTG GACCTTGTC AGGTAGAATA AGAGGTGTGT TCACATAGAT AATTTTGT			1551
CCATAAAAAA AAATGCACTG TAAGAATTAT GTCAAGGCCT AGGAGCAGGC TCAGAGTACA			1611
AGAGCTGTCC TTGCCAAAGG TCACTAAGGC AGGAACCGCA GAGCCAGCCA CCAGAGTCTT			1671

GGTACTGGGT TGAGCCCCCTC ACTATTCCCA GCACAGGGCC TGGCCCTGAG GTAAGCCTGT	1731
GCTGCTTCAG AAGTTGGCTT TTCTCCTTCT GGGATTGGTG TCCACTCTGC CCCTTTCTA	1791
GGTCATGGAG CTAGTGCAGT GTAATGTTCC CAGGAGGTAG GTACACTCTT AGGTGTTGTG	1851
GGGATCCAAG TGCTGGTTCC CACCATTGGC ATTAACAGTG GACTGCAAGC AGAGAGAGGG	1911
GTCCCCATCA TTGTTTCGTG GACACTGAGG CCTTGAGACC TTGGCTGCTG TGTCTATGTG	1971
GACTGGCAAA GACTGTGGCT TGGGAGGGC TTCCTCAGCA CTGGCACCTG AACTCAGCAC	2031
CAAGGATGGC CCCAAGAGGC TTGTTTCAT TTGCCTTGT TCTCCAGTGC TTTGGTTACC	2091
TCAGGGCAGG GCTGAACAAT AGTGTGATGT TACATTGAAG AATAAAAGACC CAACCAACAA	2151
ATGTTAGTGT CATTTTCAGT CTAAGTAAAT AAGCCATTAT GTCATTTCCC TTACTTCCTA	2211
GTAAAGTTAT GTAATTACAT AATGTAAAAA	2241

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Arg Ala Phe His Gln Thr Cys Pro Asn Phe Val Ile Glu Lys Ile Glu			
1	5	10	15
Arg Ile Gln Asn Pro Ala Leu Trp Arg Arg Tyr Gln Ala Tyr Lys Lys			
20	25	30	
Ile Met Asp Glu Lys Asn Gly Asn Val Ile Asn Glu Lys Gln Leu Phe			
35	40	45	
His Gly Thr Glu Phe Gly Ser Leu Ala Gln Leu Asn Ser Asn Gly Phe			
50	55	60	
Asn Arg Ser Tyr Ala Gly Lys Asn Ala Thr Ala Tyr Gly Lys Gly Thr			
65	70	75	80
Tyr Phe Ala Val Asn Ala Ser Tyr Ser Ala His Asp Thr Tyr Ser Lys			
85	90	95	
Pro Asp Ala Asn Gly Lys Lys Tyr Met Tyr Tyr Val Arg Val Leu Thr			
100	105	110	
Gly Asn Tyr Thr Gln Gly Asn Ala Ser Leu Ile Val Pro Pro Ser Arg			
115	120	125	
Asp Pro Gln Asn Ala Thr Asp Leu Phe Asp Thr Val Ala Asp Asn Val			
130	135	140	
Ile Asn Pro Ser Ile Phe Val Val Phe Tyr Asp Asn Gln Ala Tyr Pro			
145	150	155	160

Glu Tyr Leu Ile Thr Phe Arg Lys
165

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1918 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: HW049
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: complement (1289..1612)
 - (D) OTHER INFORMATION: /label= SAC_24337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GTGACGTGG TGATTATCTT AAAGGTAAGG GAGGTTTTTT TTTCCCTGAT ACTGATGAAG	60
GCTGAGTGTG ACTGTTTAGT ATAGCTAGTG GGCTTGTCA CTTAACGCCTT CCTTAGCATG	120
TTCCCTTCC CTTATTTTC CTGGATACTT ACGTGCTAAC GTGCTAACAA CTCCAGATCA	180
AACTGAGTAT GGAGATTTTT GCTTTAACAA TTTAGGAGTG GCAAACAATT TATAACTGGC	240
AGGGTTTGAG GACAGCCGTG TTGAAAAACC AAAAGAAAAT GCTAAGGCAG GTCTTGACCA	300
ATGTGGATAAC TTTGACTAAT TAACTTCGTT ACTTTAGGAG GAGGTTGTTCT CGCACGCCA	360
TCCATCTCCA GCGTCGAAG GTTAGATTGT TGGGGTGGTG TGTCTGTTT ACCAGATTGG	420
CTGTTCTGT GATGAATCAA CTAGCTCACT ATGACTGCTA ATGAAAACAC TGGAACACCT	480
GAGAAACTGA AGGGTGGCGT GTTGGGGCAA GGGTGCTTAC ATATCAAGCC TTTTCAATAG	540
TTTGTGTTTC TCCAGGTTCT GTTAGCAGTG CTGTTACTTG GTGCTTCAGA GGTAAAGTAAT	600
TGCAGCCAGC GTGCAGTGGT GTGCACACTG CTGGACTCAG GTCCTAACGTA CTTCATATAT	660
ATGATGACTT TCATAGAAC TCGTTGGCT GATGATTGCT GTTGAGACTT GGAAATCTGA	720
TTTTTCTGAG GATGATGGGT TGGATGGAA CAATCTGCCA GGATTTTAA CATTGCCCAT	780
CTCGTGTGTT TCAGATATGG TGAATGGCCG AGCGCAAAGG AGCCATGCCA GGTAAATGTT	840
CTAGCAATAT TATTGTTAT TAGGTAGATA CGTAATGGCT TGATCCAGTG CTTTCCTGCT	900
CACCCGTATG AACTGAATAC CGCCCCAGTC TGATAGCTGT GGAGAAAGGT ATTTTCTGAG	960
TTGAGCTCAT CTTGGATCAA ACAGGAAGGG TTTTATGCTA GTTAGTATAT GATCTCTGTA	1020

GGATACGTTT AGGCAATAAG GATAATGACC CAAATTATT TACTGTTTG CAGGAAA	1080
AAGAGCACAT CTTCATAAAG TCCAGGCTAA AGTAAGGTGA GAAAACTAAG ATGTAAAGTG	1140
TACCAAGTTA GTAACTTCCC TATGAAGAAA CATTACACG TCTTACTTCC TGTCTAGCT	1200
CCAGAGCCTG AAAAGGTGAA CCCACTGGGG CTGGCTGGGG GAAAAGAGGA AATTTGTT	1260
CAGAAGGAAC TGTCTGAGGG ATCATTGTA TGTGTGGAAA GGGAGAATT AAACTTGAT	1320
TAAAAAGGAA ACAAGGTGGT TTGTCTGTTT TTCAGGTCTG AGGAGAGGGA TGAGGTGT	1380
GTTAGAGGTA GGTAGCCCTT CAAGTCATTG TAATTAGGTG GGCAGGGTAG ATTTGCTT	1440
CTGCTAATTA AAACTTTAC CTTACAGGAA CTGAAATCAA AGATCCGATT ACCTAGGCCA	1500
GTGGCACGGC AAACCTCAGA ACTCATGGAA TACAGCCTGT TGATTCCCTG TGGATTTTA	1560
GCATCTGAGC AGTATCAGTG GCACTCCAAG TGAAATGGTT GATCTCTCA GTACCGCTGG	1620
AGCAGATTAA TATTATTTTC ACTGCCAGAG GCTATATTTTC TCTGCCCCCCC CATACCCCCT	1680
TCCTCTTCTC CTTAGACTAC TTAAGATTGA AATATTGCA ACTCCAAATT TATCTTCCTT	1740
GCTTACCACT TTTTTTCCG AGCTGGGGAC CAAACCCAGG GCCTTGCCT TCCTAGGTA	1800
GCGCTCTATC ACTGAGCTAA ATCCCCAGCC CCGCTTACCA CATTGTTAAT CTGATCCTTC	1860
CGCAGTTATT TGTGCTGTT TCCTTGTTC TGGCAATAAA TGCTTTTAT GCTAAAAA	1918

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3942 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HW050

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..1326

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: complement (3542..3733)
- (D) OTHER INFORMATION: /label= SAC_24644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTGAC ATA AAT ATG GCC GTC CGG GTA CCC CTC GGC TGC ACG GGC TCC	48
Ile Asn Met Ala Val Arg Val Pro Leu Gly Cys Thr Gly Ser	

1	5	10
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TTC TGC CCG CGG CTG CTA CCA CTG CTG GCA TTG TTG GAG CTG CTC GTC	96
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Phe	Cys	Pro	Arg	Leu	Leu	Pro	Leu	Leu	Ala	Leu	Leu	Glu	Leu	Leu	Val	
15				20					25				30			
GAC CCC AGC TTG GGC CGC GTC CAT CAC CTG GCG CTC AAA GAT GAC GTG															144	
Asp	Pro	Ser	Leu	Gly	Arg	Val	His	His	Leu	Ala	Leu	Lys	Asp	Asp	Val	
				35					40				45			
CGG CAC AAA GTC CAT CTC AAC ACC TTC GGC TTC TTC AAG GAC GGG TAC															192	
Arg	His	Lys	Val	His	Leu	Asn	Thr	Phe	Gly	Phe	Phe	Lys	Asp	Gly	Tyr	
				50					55				60			
ATG GTG GTC AAC ATC AGC AGC CTC TCT GTG AAC GAG CCT GAG GGA GTC															240	
Met	Val	Val	Asn	Ile	Ser	Ser	Leu	Ser	Val	Asn	Glu	Pro	Glu	Gly	Val	
				65					70				75			
AAG GAC AAA GAC ACT GAG ATT GGC TTC AGT CTT GAT CGG ACC AAG AAT															288	
Lys	Asp	Lys	Asp	Thr	Glu	Ile	Gly	Phe	Ser	Leu	Asp	Arg	Thr	Lys	Asn	
				80					85				90			
GAT GGC TTT TCT TCT TAC CTG GAT GAA GAT GTG AAT TAC TGT ATT TTA															336	
Asp	Gly	Phe	Ser	Ser	Tyr	Leu	Asp	Glu	Asp	Val	Asn	Tyr	Cys	Ile	Leu	
				95					100				105			110
AAA AAA AAG TCC ATG TCT TCT GTC ACT CTG CTC ATC TTA GAC ATC TCC															384	
Lys	Lys	Lys	Ser	Met	Ser	Ser	Val	Thr	Leu	Leu	Ile	Leu	Asp	Ile	Ser	
				115					120				125			
GGA AGT GGA GTC AAG GTC AGA TCC CCA CCA GAA GCT GGC AAG CAG TTA															432	
Gly	Ser	Gly	Val	Lys	Val	Arg	Ser	Pro	Pro	Glu	Ala	Gly	Lys	Gln	Leu	
				130					135				140			
CCC GAG ATT GTC TTC AGC AAG GAT GAG AAA GTC CCG AGT CGG AGC CAG															480	
Pro	Glu	Ile	Val	Phe	Ser	Lys	Asp	Glu	Lys	Val	Pro	Ser	Arg	Ser	Gln	
				145					150				155			
GAG CCT GTC AGC TCC AAC CCC AAA GAC AGC AAG GTG CAG AGA ACC															528	
Glu	Pro	Ala	Val	Ser	Ser	Asn	Pro	Lys	Asp	Ser	Lys	Val	Gln	Arg	Thr	
				160					165				170			
CCT GAT GGT TCC AAG GCT CAA CGA AGT ACA GTG GAT TCA AAG ACT ATA															576	
Pro	Asp	Gly	Ser	Lys	Ala	Gln	Arg	Ser	Thr	Val	Asp	Ser	Lys	Thr	Ile	
				175					180				185			190
GCA GAG AAA TTC TTC TCA ATT CAT AAG AAT GAT GGG GCA GTT TCA TTT															624	
Ala	Glu	Lys	Phe	Ser	Ile	His	Lys	Asn	Asp	Gly	Ala	Val	Ser	Phe		
				195					200				205			
CAG TTC TTC TTT AAC ATC AGC ACC AGT GAC CAG GAA GGC CTC TAC AGC															672	
Gln	Phe	Phe	Asn	Ile	Ser	Thr	Ser	Asp	Gln	Glu	Gly	Leu	Tyr	Ser		
				210					215				220			
CTT TAC TTC CAC AAG TGC CCA AGC AGC AAG CTG AGG TCT GGT GAG CAG															720	
Leu	Tyr	Phe	His	Lys	Cys	Pro	Ser	Ser	Lys	Leu	Arg	Ser	Gly	Glu	Gln	
				225					230				235			
GTC TCA TTC AGC CTA AAT ATT GAT ATC ACC GAG AAG AAT CCT GAC AGC															768	
Val	Ser	Phe	Ser	Leu	Asn	Ile	Asp	Ile	Thr	Glu	Lys	Asn	Pro	Asp	Ser	
				240					245				250			
TAC CTG TCT GCA GGG GAA ATC CCT CTC CCC AAG TTA TAC GTT TCC ATG															816	
Tyr	Leu	Ser	Ala	Gly	Glu	Ile	Pro	Leu	Pro	Lys	Leu	Tyr	Val	Ser	Met	
				255					260				265			270

GCC TTG TTG TTC TTC CTG TCT GGG ACC GTG TGG ATT CAC ATC CTT CGT Ala Leu Leu Phe Phe Leu Ser Gly Thr Val Trp Ile His Ile Leu Arg 275 280 285	864
AAA CGA AGG AAT GAT GTA TTT AAA ATT CAC TGG TTG ATG GCC GCC CTT Lys Arg Arg Asn Asp Val Phe Lys Ile His Trp Leu Met Ala Ala Leu 290 295 300	912
CCT TTC ACC AAG TCT CTC TCC TTG GTG TTC CAT GCA ATC GAC TAC CAC Pro Phe Thr Lys Ser Leu Ser Leu Val Phe His Ala Ile Asp Tyr His 305 310 315	960
TAC ATC TCC TCG CAG GGC TTT CCG ATT GAA GGC TGG GCT GTT GTG TAC Tyr Ile Ser Ser Gln Gly Phe Pro Ile Glu Gly Trp Ala Val Val Tyr 320 325 330	1008
TAC ATA ACT CAC CTG CTG AAG GGT GCA CTG CTG TTC ATC ACC ATC GCC Tyr Ile Thr His Leu Leu Lys Gly Ala Leu Leu Phe Ile Thr Ile Ala 335 340 345 350	1056
CTC ATT GGC ACT GGC TGG GCC TTC ATC AAG CAC ATC CTG TCT GAT AAG Leu Ile Gly Thr Gly Trp Ala Phe Ile Lys His Ile Leu Ser Asp Lys 355 360 365	1104
GAC AAG AAG ATC TTC ATG ATT GTC ATT CCG CTC CAG GTA CTG GCG AAT Asp Lys Lys Ile Phe Met Ile Val Ile Pro Leu Gln Val Leu Ala Asn 370 375 380	1152
GTG GCC TAC ATC ATA GAG TCT ACT GAG GAG GGC ACA ACT GAG TAT Val Ala Tyr Ile Ile Glu Ser Thr Glu Glu Gly Thr Thr Glu Tyr 385 390 395	1200
GGC TTG TGG AAG GAC TCT CTA TTC CTG GTG GAT TTG CTG TGC TGC GGC Gly Leu Trp Lys Asp Ser Leu Phe Leu Val Asp Leu Leu Cys Cys Gly 400 405 410	1248
GCC ATC CTC TTC CCA GTG GTG TGG TCA ATC AGG CAT TTA CAA GAA GCC Ala Ile Leu Phe Pro Val Val Trp Ser Ile Arg His Leu Gln Glu Ala 415 420 425 430	1296
TCG GCC ACA GAT GGA AAG CTG CCA TTA ACC TAGCAAAGCT GAAGCTTTTC Ser Ala Thr Asp Gly Lys Leu Pro Leu Thr 435 440	1346
AGACATTACT ACGTCCTGAT CGTGTGCTAC ATCTACTTCA CCAGGATCAT CGCCTTTCTT	1406
CTCAAGTCG CTGTTCCCTT CCAGTGGAAAG TGGCTCTACC AGCTGCTGGAA TGAAACAGCC	1466
ACACTGGTGT TCTTTGTCCT GACGGGGTAT AAATTCGCC CAGCTTCAGA TAACCCCTAC	1526
CTGCAGCTCT CTCAGGAAGA AGATGACCTG GAGATGGAGT CTGTAGTGAC GACGTCAGGA	1586
GTAATGGAGA ACATGAAGAAA GGTGAAGAAA GTGAGCAATG GTGCTGTGGA GCCCCAGGGC	1646
AGCTGGGAAG GCACCGCGTG ACAGCGCAGC TGAGGACCGC AGGCCGTCAA TGAACCTAGC	1706
TTATCCATAG CCCTATCAGT GAGCACGCC GTCCTGACA GACGATGGCA TCTCCCAGCA	1766
GCGACACCCC GGCGCTCAGC ACCATGGCCG AGCCGAGTGC TATGGACACA CACTTTGTA	1826
CTCTTAGGGA TCTGGATTGA GGTGGGCTAC AGGCAGTGAG GACTGCCCTC AGTGAGGGCG	1886
GAGGCTTAGA GGAGGAGTAA AGACTGTCTG TCTGATTTAC CTTGCTAATT GGGAGCCTGG	1946

GTCTGTGCAG GGGAGCCCCC AGTGGCTGCT ACTCAGAAAG GCTGTGGGTG TGGCACGGGT	2006
CTGCCACTCG CTGGTCACAG TTCTGTGGAG GCTGGGAGGA TGTGACTCAC TGCTTGGCCT	2066
AGCATTACG AGGCTTTGGG TTCAATTCCCT AGTGCCAGGG TGGGGGGAAA AGAAGTTACT	2126
TTGGGACTAG TCAGGTATCT ACCAAGGGCA CAGAGAAGAG AAAGAGATTG TCAGCCTTG	2186
GGAACAAGAA CAACAGAAAT GATTGAAATT CTTTTAAATA GCCAATAAAC CCCTAGGTGG	2246
CAGAAGACAC CTGTCAGGG TCACGGCCC CCAGGCACCA CTCTAAATGT CCCTGCCCC	2306
GATGTGACCT ACAACAGTGG TGCTAGAGGC CAGAGGGAGG GAGGGAGGGG GCCTGTTACA	2366
TGGCTGGCTG CAGGGGAGAA GAGCCTTGGC TCTCCAGAAG TGTCTCCAG TTGGCTCTCA	2426
GGACTCCATC CCCTGGCTGC CTGCCCAGAG CAGCCGCCTG GCTTCCTCTC CTTCCACCTG	2486
TGTCTTCTGA TCCGAGAAAA CAGTTTCCT GAAGGAGCAG CCGAGGACAG AAAGGGTAGT	2546
CTCTAAACAA ACACCTAGGT TAAGCATCTT CCACAGCTCG CATGGGCCAG GCAGGACCTC	2606
TGAGCCTCAG CTATAGTCCA AGCATGCGTG AAGGAAGTGT TTGAGCCACT CATGCTCAGA	2666
GACCTGAGGC AGCCGGTCT GCTCAGAGCT TGGACAGGGA CACCAGCGGC ACCTGCGGAA	2726
GGCCTGTGAG GGGCCACAGG AGACCAGCTC AGCACCTCAG AGCTGCTGCC TGCCCAGAAC	2786
TGGCGGGCGA GTTGCACCTT CAAGGAACAG GCACTTCCGG GAGGGGGGTG AGTTACTCCA	2846
CCTCCCAGTG CAGAAGACAA AGGTCTGGTC TCCACACCAC ACCCCAAGTC CCTGTCCTGT	2906
GCCACCAGTG AGAAGCTGCT GTCTGCTGCC CTAGCAGGTC CGTCACTACC GCAGGTGCTC	2966
CATCTTGAGA AAGGTCGACA GGCCTGAAGG ATCCACCTAA AGGACCTTTT TCTCCTGTTT	3026
TGTTTGCTTT GTTTATACTT GTTTAAAGTA TGTGGTGGGA AGGGAGTGT GAGGAGACAA	3086
GGTGTAAATG CTTTGTCTTC TGCACATAAG CACTCCTCCA GCACTGCAGA AGTGTGTCCC	3146
TGTGGTGAAT CTAAGCCACA GCTGTCCCTC AGAGGGCGCG ATCTTTATGG AAGGAGCCTC	3206
CTTTCACTTG CTGGTTTTTA ATAAGGCCAC TCTGACAGAG AGCAGAGGGG GCTGTGTACA	3266
ACCCAGCCAC AGAGCTCTCT GGGTGCACAG CTGAGCGGCT ATGGGAGACA GCCCCCTCCT	3326
TCCAGAGCAT GGGTGCACAG GCAGGGAGGT GTGCTACAGC AGCGGCCCTC CCAAGTCCTG	3386
CCCTGTGACT GCTGTAGGTG GGAAGCCAGG CATGTTGGGG GTTGTGGTGG GGAGGGGGGA	3446
TCAGAAGCCT AACATGGGGC TGGGAAGAAC TGGCCTGGTG CCCAGGCTGT GGAAAGGAAA	3506
ACTCCCAGCC CTCAGCATGC ACTGTAAGGT GTCTGTCTCA TCTGCATCGC TTGAGAGCTG	3566
GGAGCCCGCA TTCAGCAGTG TCCCTGGTA GAGGAGTCTG ATTGGCATCC AGCCGCCCA	3626
GTTCATGAGC TGCCCTCTGC AGCCTTGAGT CTTAGCCTAC CCAGCTCCAC AACCGTGT	3686
GAGTGGTGAA GCCCTTGTGT TGGAGGGGCT GAGCAGAAAT GGGGTGTACA TTGCACTGCC	3746
ACTGTGGTAT TAATAGCTCT GTGTTGTGT CCCACCCCCA CCCCCCATCT TCTGCCTGCG	3806

TGAGGTATCC ATACTTGT TT TGAGAGTGCT GTGGACTGGA AGCTGTGGGC TGTGACATTT	3866
AATAAAAGTGT GGATTTTGT AGATAATTAT TTCTTGGACA ACAGGAACAA GTGTTCAGCT	3926
CTGAAAAAAA GTCGAC	3942

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ile Asn Met Ala Val Arg Val Pro Leu Gly Cys Thr Gly Ser Phe Cys	
1 5 10 15	
Pro Arg Leu Leu Pro Leu Leu Ala Leu Leu Glu Leu Leu Val Asp Pro	
20 25 30	
Ser Leu Gly Arg Val His His Leu Ala Leu Lys Asp Asp Val Arg His	
35 40 45	
Lys Val His Leu Asn Thr Phe Gly Phe Phe Lys Asp Gly Tyr Met Val	
50 55 60	
Val Asn Ile Ser Ser Leu Ser Val Asn Glu Pro Glu Gly Val Lys Asp	
65 70 75 80	
Lys Asp Thr Glu Ile Gly Phe Ser Leu Asp Arg Thr Lys Asn Asp Gly	
85 90 95	
Phe Ser Ser Tyr Leu Asp Glu Asp Val Asn Tyr Cys Ile Leu Lys Lys	
100 105 110	
Lys Ser Met Ser Ser Val Thr Leu Leu Ile Leu Asp Ile Ser Gly Ser	
115 120 125	
Gly Val Lys Val Arg Ser Pro Pro Glu Ala Gly Lys Gln Leu Pro Glu	
130 135 140	
Ile Val Phe Ser Lys Asp Glu Lys Val Pro Ser Arg Ser Gln Glu Pro	
145 150 155 160	
Ala Val Ser Ser Asn Pro Lys Asp Ser Lys Val Gln Arg Thr Pro Asp	
165 170 175	
Gly Ser Lys Ala Gln Arg Ser Thr Val Asp Ser Lys Thr Ile Ala Glu	
180 185 190	
Lys Phe Phe Ser Ile His Lys Asn Asp Gly Ala Val Ser Phe Gln Phe	
195 200 205	
Phe Phe Asn Ile Ser Thr Ser Asp Gln Glu Gly Leu Tyr Ser Leu Tyr	
210 215 220	
Phe His Lys Cys Pro Ser Ser Lys Leu Arg Ser Gly Glu Gln Val Ser	
225 230 235 240	

Phe Ser Leu Asn Ile Asp Ile Thr Glu Lys Asn Pro Asp Ser Tyr Leu
 245 250 255

Ser Ala Gly Glu Ile Pro Leu Pro Lys Leu Tyr Val Ser Met Ala Leu
 260 265 270

Leu Phe Phe Leu Ser Gly Thr Val Trp Ile His Ile Leu Arg Lys Arg
 275 280 285

Arg Asn Asp Val Phe Lys Ile His Trp Leu Met Ala Ala Leu Pro Phe
 290 295 300

Thr Lys Ser Leu Ser Leu Val Phe His Ala Ile Asp Tyr His Tyr Ile
 305 310 315 320

Ser Ser Gln Gly Phe Pro Ile Glu Gly Trp Ala Val Val Tyr Tyr Ile
 325 330 335

Thr His Leu Leu Lys Gly Ala Leu Leu Phe Ile Thr Ile Ala Leu Ile
 340 345 350

Gly Thr Gly Trp Ala Phe Ile Lys His Ile Leu Ser Asp Lys Asp Lys
 355 360 365

Lys Ile Phe Met Ile Val Ile Pro Leu Gln Val Leu Ala Asn Val Ala
 370 375 380

Tyr Ile Ile Ile Glu Ser Thr Glu Glu Gly Thr Thr Glu Tyr Gly Leu
 385 390 395 400

Trp Lys Asp Ser Leu Phe Leu Val Asp Leu Leu Cys Cys Gly Ala Ile
 405 410 415

Leu Phe Pro Val Val Trp Ser Ile Arg His Leu Gln Glu Ala Ser Ala
 420 425 430

Thr Asp Gly Lys Leu Pro Leu Thr
 435 440

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1838 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HW051

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 114..1505

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1411..1603
 (D) OTHER INFORMATION: /label= SAC_24170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GTCGACGGCT GGTTTAAAAA GTGACAACGG CCGGTGGATT TTAGGAGTTT GCTCGGTTG	60
TAACTGCTCT TTGGTGAGCT ACTGGGACTG CAGACTAGGA GGAGACTCCC AAA ATG Met 1	116
GAA ACT CTG TCC TTC CCC AGA TAC AAC ATA GCT GAG ATT GTA GTT CAT Glu Thr Leu Ser Phe Pro Arg Tyr Asn Ile Ala Glu Ile Val Val His 5 10 15	164
ATT CGC AAT AAA CTG TTA ACT GGA GCG GAT GGC AAA AAC CTC TCC AAG Ile Arg Asn Lys Leu Leu Thr Gly Ala Asp Gly Lys Asn Leu Ser Lys 20 25 30	212
AGC GAT TTT CTT CCA AAC CCG AAG CCT GAA GTC CTG TAC ATG ATT TAC Ser Asp Phe Leu Pro Asn Pro Lys Pro Glu Val Leu Tyr Met Ile Tyr 35 40 45	260
ATG AGA GCC TTA CAG TTA GTG TAT GGG GTC CCG CTG GAG CAT TTC TAC Met Arg Ala Leu Gln Leu Val Tyr Gly Val Arg Leu Glu His Phe Tyr 50 55 60 65	308
ATG ATG CCG GTG AAC ATA GAA GTC ATG TAT CCA CAT ATA ATG GAG GGC Met Met Pro Val Asn Ile Glu Val Met Tyr Pro His Ile Met Glu Gly 70 75 80	356
TTC TTA CCG GTC AGC AAT TTG TTC TTC CAC CTG GAC TCG TTT ATG CCC Phe Leu Pro Val Ser Asn Leu Phe Phe His Leu Asp Ser Phe Met Pro 85 90 95	404
ATT TGC CGG GTG AAT GAC TTT GAG ATC GCC GAT ATT CTT TAT CCA AAA Ile Cys Arg Val Asn Asp Phe Glu Ile Ala Asp Ile Leu Tyr Pro Lys 100 105 110	452
GCA AAC CGG ACA AGT CGT TTT TTA AGT GGC ATT ATC AAC TTT ATT CAC Ala Asn Arg Thr Ser Arg Phe Leu Ser Gly Ile Ile Asn Phe Ile His 115 120 125	500
TTC AGA GAA ACA TGC CTG GAG AAG TAT GAA GAA TTT CTT TTG CAA AAT Phe Arg Glu Thr Cys Leu Glu Lys Tyr Glu Glu Phe Leu Leu Gln Asn 130 135 140 145	548
AAA TCC TCT GTG GAC AAA ATA CAG CAG TTA AGC AAT GCA CAC CAG GAA Lys Ser Ser Val Asp Lys Ile Gln Gln Leu Ser Asn Ala His Gln Glu 150 155 160	596
GCA TTG ATG AAA CTG GAA AAA CTC AAT TCG GTT CCC GTG GAG GAG CAG Ala Leu Met Lys Leu Glu Lys Leu Asn Ser Val Pro Val Glu Glu Gln 165 170 175	644
GAA GAG TTC AAA CAG CTG AAG GAT GAC ATC CAG GAG CTG CAG CAC TTG Glu Glu Phe Lys Gln Leu Lys Asp Asp Ile Gln Glu Leu Gln His Leu 180 185 190	692
CTG AAT CAA GAC TTC AGA CAG AAA ACG ACA CTG CTG CAG GAG AGA TAT Leu Asn Gln Asp Phe Arg Gln Lys Thr Thr Leu Leu Gln Glu Arg Tyr 195 200 205	740
ACC AAA ATG AAA TCA GAT TTT TCA GAG AAA ACC AAG CAT GTT AAT GAG	788

Thr Lys Met Lys Ser Asp Phe Ser Glu Lys Thr Lys His Val Asn Glu		
210 215 220 225		
CTA AAG TTG TCA GTA GTT TCT TTG AAA GAA GTT CAA GAC AGT TTG AAA		836
Leu Lys Leu Ser Val Val Ser Leu Lys Glu Val Gln Asp Ser Leu Lys		
230 235 240		
AGC AAA ATT GTG GAT TCT CCA GAG AAG CTG AAC TAT AAA GAG AAG		884
Ser Lys Ile Val Asp Ser Pro Glu Lys Leu Lys Asn Tyr Lys Glu Lys		
245 250 255		
ATG AAG GAC ACC GTC CAG AAG CTC CGC AGT GCC AGG GAA GAA GTG ATG		932
Met Lys Asp Thr Val Gln Lys Leu Arg Ser Ala Arg Glu Glu Val Met		
260 265 270		
GAG AAG TAT GAT ATC TAT AGA GAT TCT GTG GAT TGC TTG CCT TCC TGT		980
Glu Lys Tyr Asp Ile Tyr Arg Asp Ser Val Asp Cys Leu Pro Ser Cys		
275 280 285		
CAG CTG GAG GTG CAG TTA TAT CAA AAG AAA TCA CAG GAC CTT GCA GAT		1028
Gln Leu Glu Val Gln Leu Tyr Gln Lys Lys Ser Gln Asp Leu Ala Asp		
290 295 300 305		
AAT AGG GAG AAA CTA AGC AGT ATC TTA AAG GAG AGC CTG AAC CTG GAG		1076
Asn Arg Glu Lys Leu Ser Ser Ile Leu Lys Glu Ser Leu Asn Leu Glu		
310 315 320		
GGC CAG ATT GAT AGT GAT TCA TCA GAA CTA AAG AAA CTG AAG ACT GAA		1124
Gly Gln Ile Asp Ser Asp Ser Ser Glu Leu Lys Lys Leu Lys Thr Glu		
325 330 335		
GAG AAC TCC CTC ATA AGA CTG ATG ACT CTA AAG AAG GAG AGA CTT GCT		1172
Glu Asn Ser Leu Ile Arg Leu Met Thr Leu Lys Lys Glu Arg Leu Ala		
340 345 350		
ACC ATG CAG TTC AAA ATA AAC AAG AAG CAG GAG GAT GTG AAA CAG TAC		1220
Thr Met Gln Phe Lys Ile Asn Lys Lys Gln Glu Asp Val Lys Gln Tyr		
355 360 365		
AAG CGG ACC ATG ATT GAA GAT TGC AAT AAA GTT CAA GAA AAA AGA GAT		1268
Lys Arg Thr Met Ile Glu Asp Cys Asn Lys Val Gln Glu Lys Arg Asp		
370 375 380 385		
GCT GTC TGC GAG CAA GTA ACC GCC ATT AAT CAA GAC ATC CAC AAG ATT		1316
Ala Val Cys Glu Gln Val Thr Ala Ile Asn Gln Asp Ile His Lys Ile		
390 395 400		
AAA TCT GGG ATT CAG CAG CTA AGA GAC GCC GAA AAA CGG GAG AAA CTG		1364
Lys Ser Gly Ile Gln Gln Leu Arg Asp Ala Glu Lys Arg Glu Lys Leu		
405 410 415		
AAG TCT CAG GAA ATC TTG GTA GAC TTG AAA AGT GCT TTG GAG AAG TAC		1412
Lys Ser Gln Glu Ile Leu Val Asp Leu Lys Ser Ala Leu Glu Lys Tyr		
420 425 430		
CAT GAG GGC ATC GAG AAG ACG ACG GAG TGC TGC ACT AGA ATA GGA		1460
His Glu Gly Ile Glu Lys Thr Thr Glu Glu Cys Cys Thr Arg Ile Gly		
435 440 445		
GGG AAG ACT GCC GAG CTG AAG AGG AGG ATG TTC AAA ATG CCG CCC		1505
Gly Lys Thr Ala Glu Leu Lys Arg Arg Met Phe Lys Met Pro Pro		
450 455 460		

TGATCAACAG CCACCCGAAA ATGGCCTTTC GCTTTCTGTT TGGAGTAGTT ATATTGAAGC	1565
TAATAGAAGG ACCGCAGTCT CAGCTAACTA GCGTGGGTAC CATTGGTTCT CTGTCCTTTT	1625
ATGACCATGT GCTCCCTGTG TTTTTTTCTT GGTGATGGGG ATACAACCTCA GGGCCTTGCA	1685
GGCTACACTG ACTTGCCTCC CTAGGCTCTA ATGTACCATG TACTATGTAG GCTTTTGCTA	1745
CAATTAAGT AACGTGTACA GCTTTTATGT CCCTACTCTG TCTCCTTTG TATGTGCTGG	1805
TTGGAATAAA CAAATAGTTA CTGACGTCAA AAA	1838

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 464 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45;

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

.u Thr Leu Ser Phe Pro Arg Tyr Asn Ile Al

Tyr Thr Lys Met Lys Ser Asp Phe Ser Glu Lys Thr Lys His Val Asn
 210 215 220
 Glu Leu Lys Leu Ser Val Val Ser Leu Lys Glu Val Gln Asp Ser Leu
 225 230 235 240
 Lys Ser Lys Ile Val Asp Ser Pro Glu Lys Leu Lys Asn Tyr Lys Glu
 245 250 255
 Lys Met Lys Asp Thr Val Gln Lys Leu Arg Ser Ala Arg Glu Glu Val
 260 265 270
 Met Glu Lys Tyr Asp Ile Tyr Arg Asp Ser Val Asp Cys Leu Pro Ser
 275 280 285
 Cys Gln Leu Glu Val Gln Leu Tyr Gln Lys Lys Ser Gln Asp Leu Ala
 290 295 300
 Asp Asn Arg Glu Lys Leu Ser Ser Ile Leu Lys Glu Ser Leu Asn Leu
 305 310 315 320
 Glu Gly Gln Ile Asp Ser Asp Ser Ser Glu Leu Lys Lys Leu Lys Thr
 325 330 335
 Glu Glu Asn Ser Leu Ile Arg Leu Met Thr Leu Lys Lys Glu Arg Leu
 340 345 350
 Ala Thr Met Gln Phe Lys Ile Asn Lys Lys Gln Glu Asp Val Lys Gln
 355 360 365
 Tyr Lys Arg Thr Met Ile Glu Asp Cys Asn Lys Val Gln Glu Lys Arg
 370 375 380
 Asp Ala Val Cys Glu Gln Val Thr Ala Ile Asn Gln Asp Ile His Lys
 385 390 395 400
 Ile Lys Ser Gly Ile Gln Gln Leu Arg Asp Ala Glu Lys Arg Glu Lys
 405 410 415
 Leu Lys Ser Gln Glu Ile Leu Val Asp Leu Lys Ser Ala Leu Glu Lys
 420 425 430
 Tyr His Glu Gly Ile Glu Lys Thr Thr Glu Glu Cys Cys Thr Arg Ile
 435 440 445
 Gly Gly Lys Thr Ala Glu Leu Lys Arg Arg Met Phe Lys Met Pro Pro
 450 455 460

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (vii) IMMEDIATE SOURCE:

(B) CLONE: HW052

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 247..765

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: complement (660..1062)
- (D) OTHER INFORMATION: /label= SAC_24882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GTCGACCAAA AACAGGACAG ATTGCAACAG CCTCTACACT TCCTTCATGG CCTGCTCTTG	60
GGCCGTGGCG ACAAGCAGAA AGAACGCTTGA TTGTGGAGAG GTGCCCTAGC GGAGGGATGT	120
CTGCCACAGT CCAGGCACCC CACAGAGGGT AGGAGCTCCA TGTACGAGTG GCTTTGCATT	180
TCTTCAGAAA AGAATAGCTG ATGTGCAATC TCAGCCTTTC TGCAGAAGGA TTTATCAGGG	240
GCCAGC ATG GGC TCT GTG AAT TCT AGA GGC CAT AAG GCC CAG GTG GTA Met Gly Ser Val Asn Ser Arg Gly His Lys Ala Gln Val Val	288
1 5 10	
ATG CTG GGC CTC GAC TGT GCT GGC AAG ACC ACA ATC CTG TAC AAA CTG Met Leu Gly Leu Asp Cys Ala Gly Lys Thr Thr Ile Leu Tyr Lys Leu	336
15 20 25 30	
AAA GGA AAC CGG CTG GTG GAT ACC CTA CCC ACT GTT GGT TTT AAT GTA Lys Gly Asn Arg Leu Val Asp Thr Leu Pro Thr Val Gly Phe Asn Val	384
35 40 45	
GAG CCT CTT GAG GCT CCT GGA CAT GTG TCG CTG ACT CTC TGG GAC ATT Glu Pro Leu Glu Ala Pro Gly His Val Ser Leu Thr Leu Trp Asp Ile	432
50 55 60	
GGG GGA CAG ACC CAG CTC AGG GCT ACG TGG AAG GAC TAC CTG GAA GGC Gly Gly Gln Thr Gln Leu Arg Ala Thr Trp Lys Asp Tyr Leu Glu Gly	480
65 70 75	
ATT GAC CTC CTT GTG TAC GTG CTG GAC AGC ACA GAT GAA GCC CGC TTG Ile Asp Leu Leu Val Tyr Val Leu Asp Ser Thr Asp Glu Ala Arg Leu	528
80 85 90	
CCC GAG GCA CTG GCT GAG CTC GAG GAA GTC CTA GAA GAC CCC AAC ATG Pro Glu Ala Val Ala Glu Leu Glu Val Leu Glu Asp Pro Asn Met	576
95 100 105 110	
GCT GGT GTT CCT TTC TTG GTA CTG GCC AAC AAG CAG GAG GCT CCT GAT Ala Gly Val Pro Phe Leu Val Leu Ala Asn Lys Gln Glu Ala Pro Asp	624
115 120 125	
GCT CTA CCA TTG CTT GAA ATC AGA AAC AGG CTG GAC CTG GAA AGG TTC Ala Leu Pro Leu Leu Glu Ile Arg Asn Arg Leu Asp Leu Glu Arg Phe	672
130 135 140	
CAA GAC CAT TGC TGG GAG CTG CGG GCT TGC AGC GCT CTC ACA GGT CAG Gln Asp His Cys Trp Glu Leu Arg Ala Cys Ser Ala Leu Thr Gly Gln	720
145 150 155	
GGG CTA CAG GAA GCC CGG CAG AGC CTG CTG CAT TTG CTG AGA TCC	765

Gly Leu Gln Glu Ala Arg Gln Ser Leu Leu His Leu Leu Arg Ser		
160	165	170
TGATGAAATG CAGTAACCTC TAACTCCAGG CTGGAGCAGG ACAGGGAGCA GGGTCAGCCA	825	
GACCCCCCTGA GCAGGCATAAT AGATTATCCT TGCTTCTAAG AACAGGAGGG GCCAGCTGAT	885	
CCTTGAGAAA GTGAAGCTCC GTTTGCCACA TGAGAAACCA CGTTTCTCTT GGACGGTGTG	945	
TTTCTCTC AGGACTTCTT CTCAGTGGCG GTTATGCGGA AAATCAACTG TTCTTCAAGT	1005	
AACAATCGTC AGAGGAAATA TAAAAACCTT CAGAATACCC CCATGTAACA GCTCAGTACC	1065	
AAGTGTCAA GTCACAAACT TGGTGACATA ATTATTGATG ACCAAGTTCA CAAATGAAAA	1125	
GAGGTTCAA AACTACATCT GAGTGTCACT GGGCCTATCG CTGTTATCCG AGTGTCACTG	1185	
GGCCTATCAT TGTCATCCGA GTGTCACCAG GCCTATCACG GTTCATCTGCC TGTCACTGGG	1245	
CCTATCACAG TCATCAGGAG CGACTCTTCC TACTGGCCTT GGGCAGAAG CCACTGTCAC	1305	
TGGTGGGCTC ACAGCAGGAG GGGCAGGTCT GCTCTCATAA TGCTGCAGAA GGCAGAAGTC	1365	
CATGGGGCCC TAGATCCTCC CAGAATTCCC CCTGATCTCC AACTCTGACT AACTCTTTTC	1425	
TGCCCTATAT CCTCTGTTGT AAAAAAGTAA AATAAAACTC CTCTTATACT CTCAAAAAA	1483	

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met Gly Ser Val Asn Ser Arg Gly His Lys Ala Gln Val Val Met Leu			
1	5	10	15
Gly Leu Asp Cys Ala Gly Lys Thr Thr Ile Leu Tyr Lys Leu Lys Gly			
20	25	30	
Asn Arg Leu Val Asp Thr Leu Pro Thr Val Gly Phe Asn Val Glu Pro			
35	40	45	
Leu Glu Ala Pro Gly His Val Ser Leu Thr Leu Trp Asp Ile Gly Gly			
50	55	60	
Gln Thr Gln Leu Arg Ala Thr Trp Lys Asp Tyr Leu Glu Gly Ile Asp			
65	70	75	80
Leu Leu Val Tyr Val Leu Asp Ser Thr Asp Glu Ala Arg Leu Pro Glu			
85	90	95	
Ala Val Ala Glu Leu Glu Val Leu Glu Asp Pro Asn Met Ala Gly			
100	105	110	
Val Pro Phe Leu Val Leu Ala Asn Lys Gln Glu Ala Pro Asp Ala Leu			
115	120	125	

Pro Leu Leu Glu Ile Arg Asn Arg Leu Asp Leu Glu Arg Phe Gln Asp
130 135 140

His Cys Trp Glu Leu Arg Ala Cys Ser Ala Leu Thr Gly Gln Gly Leu
145 150 155 160

Gln Glu Ala Arg Gln Ser Leu Leu His Leu Leu Arg Ser
165 170

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HW054

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1952..2152
- (D) OTHER INFORMATION: /label= SAC_24183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GTGCGACGGTG GGGTCTAACT GAGGTCTTGT ATTTGGTTTT TCCTGAAGAT CGACCTCTGG	60
CATCAGGAGG CTTGAGCAAG GAGAAGAGTG GATGATGAAG GAAAGAGACA AGGAAAGAAA	120
GAGAAGTGTG CACAAAGAAA CTTGTATTAT TATTAATTAG CACCTAGCTT GTTTGTGTCT	180
GATACACCAC CAAGTAGTAA TTGTTGAAAA AAGCGAAGAA GAAAAAAA AAAACAAAAAA	240
AACCAAACAG TGGGTACTCA AATAAGATAG GAGAAAAATG AAGAGAACAG ACCCAGTTCT	300
CGACCCTTGC TTCTCGAAGG TCCTCCCACC AGGCTGCCAA AGCAAGATGG TGTTGCTCTG	360
ATCCAGTCAG TATTCTTTTG ACTTTTTTTT TTAATCTCCA GGTTTGGTT CAGGCTCCCA	420
TATTCATACC CTGGCTCATT TAGCTTCCC TCATGTTGTG GGTTCTTCTG TCCCTCACCC	480
CCTTACTCTC CCCACTGATA TTCTTCCCAC GTCAAGACTG TGGCTCTGGA AGAAATATCC	540
ACCATTGCA GAGCTGATGT TCTGTAGATC GTAATGTTGA AGCGCTGGGT GTCCCTGGTTG	600
GCAGAATCAC TCCTGTATTA CTCTGGTACA TAGGTGTCTC CTGNTAGACT CCCTGGCCTT	660
AGTCATGGGG TGTTTCTAG AGGCAGACTA AGACAGGAGT CAAAAAAGAT TTAGAGGAAG	720
GAGCTGAGGA AAGAAAGACA GTTGTGGGAG GAAAATCAAG TTCTACTCAG GATCCCCAGT	780
GTTTCTGTAG ATGTAGATTG GAATGTGTCC ATAACAGAGA GGCCAGTGAG AGACATCCCC	840

AAGGACCTGC CAGGCTTCC	TTCGCTCCAG GAAGACGCAC CATCACTCAA AAGGGGTTTC	900
CTAGAAAAGAA AGACAAGTGA CTTAAAAAAT CTGCCAGTGG GTTCTTGAAG TCATCGAAC	960	
TAGGAGGTAG AAAGCTCACG GGGGTCAATGT TATCGAAGGG AGGTGAGGTT CAGTCAGGCT	1020	
AACTATTAGG GAGANTGTCA AAGGAGGCTA CAGAAATGGG ATTCTGGCTG TGGGGCATTA	1080	
AAGGCTATCA AGTCAACAGG TAAGAGTGG A GTGGCTCAGC AGCTTCTCTG GCGCTGAAAG	1140	
TGGTGCTCT TAACAGTTAA TTCCCTTCCC TTTTCCATCA CAGAAGGAAT CATTCCAGCC	1200	
CTCCCTGGGA TTATGGTCCC CCAGTGACCA TGTTCCATCT GCTGGATTT TGATCAGTT	1260	
AGAAGGAAAA AAACACTTGG GTTCGGTGGT ATTTGCTTAT GACCTTAGCA CTTTGGAGCT	1320	
GAGAAGAGGA TTGCCATAGT TTCCAGACCA GTCTGGTTA CATACTGAGT TCTAGGGCTG	1380	
CGTAATGAGA TGTCTCAAGA ATGGAGAGGG GCGTTAGGGA GAACTTACTT AGCTCTCAA	1440	
GAAACTGTCC TGAAACAAA GAGAAATGAG TCGATGGTG ACCAGTGGGA GCCTNCCCC	1500	
CACCTCCTCA GACAACCCTT CTTTCCATT AAGGGCCTG TGCATCTCAG TAAGTGGTCC	1560	
TCAGTTTCC TGAGGATTCT GATGGTGAGA GTAGAGAGAG CAAAAAGATT CTCAGCCCTG	1620	
GGATCTAGAA CCTTGGTCC ACTCTTTCC CGTTCTGGTC TGCCCTGAGCT CCCCCCCCCC	1680	
GCCCCCCAGT GGTCTGTGTT GCTGTCCAGA CATTGCACCT GCCAGTCTTC GGTGCAGCCA	1740	
GTTGTAGCAG ATGATCAAAG CAACCAGNN TCCAAGAACCA GGGACAATCA ACAAACAGTG	1800	
TTATCTTCCA GCAGGGCACT CTCAGGAAGT GAGGATCTGA ATGGTAAAGC AGAACAGAGT	1860	
GTTCCTCT ATGCCACAGC CGCTCATGCC ACACCCACTT GAAGCCTCCA AAGCCAGNAC	1920	
AAGCTGTAGA GTCCATGAAT GTAGATGAGG TACATTGTGC GCCTTGCTTT TACTTCCTT	1980	
AGCTTCTGAT TGAATTTAGC TGTATCTTT TAACCGATTT ATCGTAGAAN ACAATGGTG	2040	
GTGTGACCCCT NTCATGCTTT GTTGATCTTC AGCCACACGC TGCCCTCCCT CGCCCCCACT	2100	
TCTAGCATTG GTGTGTGTGC GCGTGTGTTTT TTGAAGAGGG GTTNTTGCTT GTACAATCCC	2160	
TGGCTGGCCT TGAACCTTGAG AAGTCCTCCT GCCTCCGCCT TCCAGGTGCT GGGATTACAA	2220	
GTTGTCAACC CTGCTTTCAC TAATGTTCC TTTTATTAA AGATTTATTT ATTATTTAAA	2280	
AAGTCGAC	2288	

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: HW055

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 214.1329

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1953..2065
(D) OTHER INFORMATION: /label= SAC_24449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

155	160	165	
CTG AGT TCC CCG TCC CTC GTC TTC CGG GAC ACG GTC AGC ACC AGC CAC Leu Ser Ser Pro Ser Leu Val Phe Arg Asp Thr Val Ser Thr Ser His 170	175	180	762
GGG AAG ATA ACC TGC TTC AAC AAC TTC AGC CTG GCC GCG CCC GAG CCT Gly Lys Ile Thr Cys Phe Asn Asn Phe Ser Leu Ala Ala Pro Glu Pro 185	190	195	810
TTC TCT CAT TCC ACC CAC CCG CGA ACA GAC CCG GTA GGG TAC AGC AGA Phe Ser His Ser Thr His Pro Arg Thr Asp Pro Val Gly Tyr Ser Arg 200	205	210	858
CAT GTG GCG GTC ACC GTC ACC CGC TTC CTC TGT GGC TTC CTG ATC CCC His Val Ala Val Thr Val Thr Arg Phe Leu Cys Gly Phe Leu Ile Pro 220	225	230	906
GTC TTC ATC ATC ACG GCC TGT TAC CTC ACC ATC GTC TTC AAG TTG CAG Val Phe Ile Ile Thr Ala Cys Tyr Leu Thr Ile Val Phe Lys Leu Gln 235	240	245	954
CGC AAC CGC CTG GCC AAG ACC AAG AAG CCC TTC AAG ATC ATC ATC ACC Arg Asn Arg Leu Ala Lys Thr Lys Lys Pro Phe Lys Ile Ile Ile Thr 250	255	260	1002
ATC ATC ATC ACC TTC TTC CTC TGC TGG TGC CCC TAC CAC ACA CTC TAC Ile Ile Ile Thr Phe Leu Cys Trp Cys Pro Tyr His Thr Leu Tyr 265	270	275	1050
CTG CTG GAG CTC CAC CAC ACG GCT GTG CCA GCC TCT GTC TTC AGC CTG Leu Leu Glu Leu His His Thr Ala Val Pro Ala Ser Val Phe Ser Leu 280	285	290	1098
GGA CTG CCC CTG GCC ACA GCC GTT GCC ATC GCC AAC AGC TGT ATG AAC Gly Leu Pro Leu Ala Thr Ala Val Ala Ile Ala Asn Ser Cys Met Asn 300	305	310	1146
CCC ATC CTG TAC GTC TTC ATG GGC CAC GAC TTC AAA AAA TTC AAG GTG Pro Ile Leu Tyr Val Phe Met Gly His Asp Phe Lys Lys Phe Lys Val 315	320	325	1194
GCC CTT TTC TCC CGC CTG GTG AAT GCC CTG AGC GAG GAC ACA GGA CCC Ala Leu Phe Ser Arg Leu Val Asn Ala Leu Ser Glu Asp Thr Gly Pro 330	335	340	1242
TCC TCC TAC CCC AGT CAC AGG AGC TTC ACC AAG ATG TCC TCA TTG ATT Ser Ser Tyr Pro Ser His Arg Ser Phe Thr Lys Met Ser Ser Leu Ile 345	350	355	1290
GAG AAG GCT TCA GTG AAT GAG AAA GAG ACC AGC ACC CTC TGAGCCTTCC Glu Lys Ala Ser Val Asn Glu Lys Glu Thr Ser Thr Leu 360	365	370	1339
CTGGGACTGT CCCCAATGGG CTCCACAGCC CAGGGACTTG TCTCCTGAGG TAGGAGACAC			1399
GCCTGGAGCC TTTGGGTATG CCCCAGCGCC CGCTACGTCT TGCGCAAGGC GGCCCATTGT			1459
TTTGGGTGGA GTTCCCAAGT GTGGACACTC TTCCAGCAAATGGCAGACA AGCAACCTGA			1519
GCCCCCTGCAG CAGGAGTATA GGACCAACTT CCACCGGCTC AGAAAAGGGA GGGTCTCTGA			1579
AACCAAGGTC TGAGCTGTGA CCCACATACA GGCACACAAAT TTCACTGTGG ATGCCCAAA			1639

CATGCTGCAC AGTCTCCAGT GTGGGTGAGG ACGTCACTGC AGACCTGTTA TGGCGACATG	1699
ACAGTCAAAC CAGCAAATAC CCCACCACCA CTGTCATCCT CCAAGATCTT GACTTTGGAT	1759
TTCAGAAAAA TGGGGAGGAC CAGGACCTGA GGGGCTTCAT AGAACTTGCT TGCAAGGGCA	1819
GCCCAGGTGT GTGTGTGTGT ATGTGCTTGT GTGTGTGTGT GTGTGTATGT GCATGTGTGT	1879
GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT AAGAGGTGGA GACAGAGAGC AGAGAACCCC	1939
AAAGGATGTG GGTACAGGAT ATCTCACACC ATCATGCCAC AGGGAGACAG AGCTACAACG	1999
ATGGGTGCTT GGGGGTTCAG ATGGTGGCAG CTCTTGCTT CAGTGTGTAT ACCCCCCCTAG	2059
CACTGTACCC CCAGGCTGGA GGGGGCTCT TCACAGAACG TTCCAACCCA TTCCAGCACT	2119
GGCTGGAAGG GCTTGGGATG TCCCTGGAGA CTGGTCTGGG ACTATCTTCA AAGCGTCTTC	2179
CAAAGGCTGC TGCTGACCAG CTCACCTGAC TCCTCCTTGA ACACACTCCC CACGTGGGC	2239
ATCACAGCCC CGATGGCAGC CCAGGATCAG GCCTCCCTCC CTTGACAGGG AAATGACTCA	2299
CCCAACCCA TGCAGTGTCA GTAACAAAGA CCCAGGCCA GCTCCAAAAA	2349

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```

Met Glu Tyr Glu Gly Tyr Asn Asp Ser Ser Ile Tyr Gly Glu Glu Tyr
 1           5           10          15

Ser Asp Gly Ser Asp Tyr Ile Val Asp Leu Glu Glu Ala Gly Pro Leu
 20          25          30

Glu Ala Lys Val Ala Glu Val Phe Leu Val Val Ile Tyr Ser Leu Val
 35          40          45

Cys Phe Leu Gly Ile Leu Gly Asn Gly Leu Val Ile Val Ile Ala Thr
 50          55          60

Phe Lys Met Lys Lys Thr Val Asn Thr Val Trp Phe Val Asn Leu Ala
 65          70          75          80

Val Ala Asp Phe Leu Phe Asn Ile Phe Leu Pro Ile His Ile Thr Tyr
 85          90          95

Ala Ala Met Asp Tyr His Trp Val Phe Gly Lys Ala Met Cys Lys Ile
100         105         110

Ser Ser Phe Leu Leu Ser His Asn Met Tyr Thr Ser Val Phe Leu Leu
115         120         125

Thr Val Ile Ser Phe Asp Arg Cys Ile Ser Val Leu Leu Pro Val Trp
130         135         140

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Ser Gln Asn His Arg Ser Val Arg Leu Ala Tyr Met Thr Cys Val Val
 145 150 155 160
 Val Trp Val Leu Ala Phe Phe Leu Ser Ser Pro Ser Leu Val Phe Arg
 165 170 175
 Asp Thr Val Ser Thr Ser His Gly Lys Ile Thr Cys Phe Asn Asn Phe
 180 185 190
 Ser Leu Ala Ala Pro Glu Pro Phe Ser His Ser Thr His Pro Arg Thr
 195 200 205
 Asp Pro Val Gly Tyr Ser Arg His Val Ala Val Thr Val Thr Arg Phe
 210 215 220
 Leu Cys Gly Phe Leu Ile Pro Val Phe Ile Ile Thr Ala Cys Tyr Leu
 225 230 235 240
 Thr Ile Val Phe Lys Leu Gln Arg Asn Arg Leu Ala Lys Thr Lys Lys
 245 250 255
 Pro Phe Lys Ile Ile Ile Thr Ile Ile Thr Phe Phe Leu Cys Trp
 260 265 270
 Cys Pro Tyr His Thr Leu Tyr Leu Leu Glu Leu His His Thr Ala Val
 275 280 285
 Pro Ala Ser Val Phe Ser Leu Gly Leu Pro Leu Ala Thr Ala Val Ala
 290 295 300
 Ile Ala Asn Ser Cys Met Asn Pro Ile Leu Tyr Val Phe Met Gly His
 305 310 315 320
 Asp Phe Lys Lys Phe Lys Val Ala Leu Phe Ser Arg Leu Val Asn Ala
 325 330 335
 Leu Ser Glu Asp Thr Gly Pro Ser Ser Tyr Pro Ser His Arg Ser Phe
 340 345 350
 Thr Lys Met Ser Ser Leu Ile Glu Lys Ala Ser Val Asn Glu Lys Glu
 355 360 365
 Thr Ser Thr Leu
 370

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2577 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: HW056
- (ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 8..523

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION: complement (738..953)
 (D) OTHER INFORMATION: /label= SAC_24326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTGCGACG GGC TAC CTT AGC CAG CTG ATG CTT CCA GTG ACA GAG CCA CTT	49
Gly Tyr Leu Ser Gln Leu Met Leu Pro Val Thr Glu Pro Leu	
1 5 10	
TGT CCT TTG CAC AGC CTG ACA CCC TAT CAG GTC CCC TTC AAT GCA GTT	97
Cys Pro Leu His Ser Leu Thr Pro Tyr Gln Val Pro Phe Asn Ala Val	
15 20 25 30	
GCT ATC CGG GTC ACG CAC GCC GAC GTT GCA CCT ACC CAC ATA CTG TAC	145
Ala Ile Arg Val Thr His Ala Asp Val Ala Pro Thr His Ile Leu Tyr	
35 40 45	
GCT ATG AAT GCC AGC TGG GTC GGC CTT TGC AAG ATT GTG GAT GAT ATG	193
Ala Met Asn Ala Ser Trp Val Gly Leu Cys Lys Ile Val Asp Asp Met	
50 55 60	
AAA GGC TAC ACT CGG GGC CCC ATT CTG CTG GCC CAG AAC CCC ATA TGT	241
Lys Gly Tyr Thr Arg Gly Pro Ile Leu Leu Ala Gln Asn Pro Ile Cys	
65 70 75	
GAC TGT TTG GGC TTT GGT ATC TGC AGA GGC ATT GAC ATG GAC AAG CGG	289
Asp Cys Leu Gly Phe Gly Ile Cys Arg Gly Ile Asp Met Asp Lys Arg	
80 85 90	
CTG TAC CAC ATC CTC ACC CCT CTA CCA CCA GAG GAG TTA AGA ACT GTG	337
Leu Tyr His Ile Leu Thr Pro Leu Pro Pro Glu Glu Leu Arg Thr Val	
95 100 105 110	
AAC TGT CTG CTG GTT GGC ACC ATT TCC ATT CCA CAT TGT ATT TTC AAG	385
Asn Cys Leu Leu Val Gly Thr Ile Ser Ile Pro His Cys Ile Phe Lys	
115 120 125	
AAT CAG CCT GGG ACT GAA GGG ACA GTT CCT TAT GTC ACC AGG GAT TAT	433
Asn Gln Pro Gly Thr Glu Gly Thr Val Pro Tyr Val Thr Arg Asp Tyr	
130 135 140	
AAT TTA AAA CTT CTT GGA GCA TCA GAG AAA ATT GGG GAG AGA GAG TAT	481
Asn Leu Lys Leu Leu Gly Ala Ser Glu Lys Ile Gly Glu Arg Glu Tyr	
145 150 155	
AGA AAT ATA CTA CCT AGA CAC AAA TCA CGG CAA AGA AGA AAA	523
Arg Asn Ile Leu Pro Arg His Lys Ser Arg Gln Arg Arg Lys	
160 165 170	
TGAAGCCTGG GTGTACAGAG AGACTTCGC CTCGACACAT TGTCCCCAAG CCTAGAGTCA	583
GCAGACTGAG CGGGCTGTGT GGCTGCTGAC CTCGTGCCA TGCCCAGTGT TCATATAACT	643
GGAAAATGTG CTGTGGTAAG AGTCATTCAA GCCCCCTCGT TTTTTTCCCC TCTAAGACAT	703
GGAGGGCCTC ATATAGCTCA GACTGGCCTC AGTACTCTGG TCCTCCTGTC TCACTGTCCA	763

AGGGCTGCGC ATCCGGCTTT TGGTCTCATA CTTGGCCCAG ACCTTGCCGA CTGGTTGTCC	823
TGGGTGTGTG GTGCTCCTGG AGAGCTGGGA AGCATTGAAG AAAGCTGTGG TGTCTCTCAA	883
GAAGACCAGG GCCACAAAAG TGTGCCTAGA AACTGAGTAG CAGGCTGACC ACAGGTTCTC	943
GGGTGCAGTG TACGGACTGG CAGGGACCTG AGCAGGCTCA GTGGCCGTGA GTAAGAGGCT	1003
TACTCCGTTG AACCTTGTGG ACCTTAGCAC CCCAGTGTGG CGGCTCATTG GCCTGATCCT	1063
TTGATGCTTG CCATCGAACATC TCCCAATGCT GCAATCAAGT GTTAGAGGAC GGTACGTCGT	1123
CTTGTAAATT TCTGGGTCTT TAATCATGAG GCTTTATGTT GAAGAACTTG CTCTGACATT	1183
CAGAAAGCCT CACGTTAGTT AAAGAAATCC ATGGTCCCT AATTCTGGGG ATGTTCTGAC	1243
AGACCTTGAG GCTGTAGATA CGTCAGAAAG CCTCCATGTT AGTTAAGGAA ATCCATGGTT	1303
CCCTTAATTCT GGGGATGTTC TGACTGGAA TGTTCTGACA GACCTTGAGG CTGAGATACT	1363
ACCATGGGCC CACTAGCCTG GGACAGGCAC ACATATGCCT GGCTTGGCA GACCTTGCT	1423
ATCAACGATT TCTTCTAAGG CCCCAGAGGC CACTGCAAGT GGATGTTGCA ATCCGGAGTG	1483
ACTGGGTCGG GTCATTTTG TGGTTGCAAA GCAGGACCT GAGGAGCCTC TTGGGCTGGC	1543
ATGATGGATC TGACAAGACT CCACCTTGCA TGGAATCAGG AAGGACCAAG GCTATGGAAG	1603
GCTCACAAACA TTGATTGTCT CCGTCTTGTC TGTAGTCATA GGAGTGTGGC CAGTCTCCTC	1663
TGCTTGGCGC CATCTTGTG TGCGCCTCAG CATCTGAAAA TCCTCCGAGG AGGCAGAGCT	1723
GCCTCTCTG GATTAGTCGG ATTCCCTGTA GATCACTCGG GCTCACAAC ACTCCCTGCC	1783
CCACCCCCAA CACCATCTCT GTCTCACTTG AGCTTGTGGT GAGCCTTGC AGAGGGGAGG	1843
AGCTCTTCCT GCCCAGGCAC TCTCTGGCT CCTGATCCTC AAGCCTCTGC TTCCCTGGTG	1903
CTCAGATCAC AGGTGTGTGC CGTCTTAGCC TTGCGGACAG TTTAAGACA GCCTTGGTCA	1963
CCTTCATCTC CCTCCCCGGG TCTTCCTGTC TTCACAATAA AGATCCCGAG TCCAAAAAAA	2023
AAAAAAAAAA AAATTCCAGG AGGAAATCTG GGTGCACAGA ACTTATCTGA GTCGGCTTTG	2083
GTGAAGGAGA TCCTCAAGGA GCAGGAGAAC AGGAAGGGCC TCATAGCTGC CATCTGTGCG	2143
GGTCCTACGG CCCTGCTGGC TCACGAAGTA GGCTTGGAT GCAAGGTTAC ATCGCACCCA	2203
TTGGCTAAGG ACAAAATGAT GAACGGCACT CACTACAGCT ACTCAGAGAG CCGTGTGGAG	2263
AAGGACGGCC TCATCCTCAC CAGCCGTGGG CCTGGGACCA GCTTCGAGTT TGCGCTGGCC	2323
ATTGTGGAGG CACTCAGTGG CAAGGACATG GCTAACCAAG TGAAGGCCCG GCTTGTCTC	2383
AAAGACTAGA GCCCAAGCCC TGGACCCCTGG ACCCCCCAGGC TGAGCAGGCA TTGGAAGCCC	2443
ACTAGTGTGT CCACAGCCCCA GTGAACCTCA GGAACAAACG TGTGAAGTAG CCCGCTGCTC	2503
AGGAATCTCG CCCTGGCTCT GTACTATTCT GAGCCTTGCT AGTAGAATAA ACAGTTCCCC	2563
AAGCTCCTGA AAAA	2577

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gly Tyr Leu Ser Gln Leu Met Leu Pro Val Thr Glu Pro Leu Cys Pro
 1 5 10 15

Leu His Ser Leu Thr Pro Tyr Gln Val Pro Phe Asn Ala Val Ala Ile
 20 25 30

Arg Val Thr His Ala Asp Val Ala Pro Thr His Ile Leu Tyr Ala Met
 35 40 45

Asn Ala Ser Trp Val Gly Leu Cys Lys Ile Val Asp Asp Met Lys Gly
 50 55 60

Tyr Thr Arg Gly Pro Ile Leu Ala Gln Asn Pro Ile Cys Asp Cys
 65 70 75 80

Leu Gly Phe Gly Ile Cys Arg Gly Ile Asp Met Asp Lys Arg Leu Tyr
 85 90 95

His Ile Leu Thr Pro Leu Pro Pro Glu Glu Leu Arg Thr Val Asn Cys
 100 105 110

Leu Leu Val Gly Thr Ile Ser Ile Pro His Cys Ile Phe Lys Asn Gln
 115 120 125

Pro Gly Thr Glu Gly Thr Val Pro Tyr Val Thr Arg Asp Tyr Asn Leu
 130 135 140

Lys Leu Leu Gly Ala Ser Glu Lys Ile Gly Glu Arg Glu Tyr Arg Asn
 145 150 155 160

Ile Leu Pro Arg His Lys Ser Arg Gln Arg Arg Lys
 165 170

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HW057

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..1023

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1032..1176
- (D) OTHER INFORMATION: /label= SAC_23926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GTCGAC GGC GCG CTG GAG GAC GCA CGG CTT GGC GGG AAG GCG AGG GGA Gly Ala Leu Glu Asp Ala Arg Leu Gly Gly Lys Ala Arg Gly 1 5 10	48
CCG TGC GGA GCC TCC GGT GCT GGC GGC CAC CAG TTC GGG AGC CGG Pro Cys Gly Ala Ser Gly Ala Gly Gly His Gln Phe Gly Ser Arg 15 20 25 30	96
GAG CCG GCC GCA GCA CGC GGA ACA GAG CAG AGG GTG GCG GGG CCC GGC Glu Pro Ala Ala Arg Gly Thr Glu Gln Arg Val Ala Gly Pro Gly 35 40 45	144
GAA ACC ACG ATG AAG CCG AAC AGC GAG GAA GAG GAG GAG TTG GTG CAG Glu Thr Thr Met Lys Pro Asn Ser Glu Glu Glu Glu Leu Val Gln 50 55 60	192
GGC GTG GGC CCC TGG GAC GAG TGC TTC GAG GTG GCC GTG CAG TTG GCG Gly Val Gly Pro Trp Asp Glu Cys Phe Glu Val Ala Val Gln Leu Ala 65 70 75	240
TTG CGT GCG GGA CAA ATC ATC AGA AAG GCC CTC ACT GAG GAA AAA CAC Leu Arg Ala Gly Gln Ile Ile Arg Lys Ala Leu Thr Glu Glu Lys His 80 85 90	288
GTC TCG ACG AAA ACA TCT GCT GCA GAT CTT GTG ACA GAA ACA GAT CAC Val Ser Thr Lys Thr Ser Ala Ala Asp Leu Val Thr Glu Thr Asp His 95 100 105 110	336
CGA GTA GAA GAC TTA ATT GTT TCT GAG TTG CGA AAG CGG TTC CCT TCA Arg Val Glu Asp Leu Ile Val Ser Glu Leu Arg Lys Arg Phe Pro Ser 115 120 125	384
CAC AGG TTC ATT GCA GAA GAG GCC ACA GCA TCC GGG GCC AAG TGT GTG His Arg Phe Ile Ala Glu Ala Thr Ala Ser Gly Ala Lys Cys Val 130 135 140	432
CTC ACC CAC AGC CCG ACC TGG ATC ATC GAC CCC ATC GAC GGC ACC TGC Leu Thr His Ser Pro Thr Trp Ile Ile Asp Pro Ile Asp Gly Thr Cys 145 150 155	480
AAC TTT GTG CAC AGA TTC CCC ACT GTG GCA GTT AGC ATC GGA TTT GCT Asn Phe Val His Arg Phe Pro Thr Val Ala Val Ser Ile Gly Phe Ala 160 165 170	528
GTT CAC CAG GAG CTG GAA TTC GGA GTG ATT CAC CAC TGC ACA GAG GAG Val His Gln Glu Leu Glu Phe Gly Val Ile His His Cys Thr Glu Glu 175 180 185 190	576
CGG CTG TAC ACC GGC AGG AGG GGC CAG GGC GCC TTT TGC AAT GGC CAG Arg Leu Tyr Thr Gly Arg Arg Gly Gln Gly Ala Phe Cys Asn Gly Gln 195 200 205	624
AGG CTC CAG GTC TCC AGG GAG ACA GAT CTC GCA AAG GCC TTG GTT CTG Arg Leu Gln Val Ser Arg Glu Thr Asp Leu Ala Lys Ala Leu Val Leu	672

210	215	220	
ACA GAA ATC GGG CCC AAA CGT GAC CCC GAT ACT CTG AAA GTA TTC CTG Thr Glu Ile Gly Pro Lys Arg Asp Pro Asp Thr Leu Lys Val Phe Leu			720
225	230	235	
AGC AAC ATG GAG CGG CTG CTG CAC GCC AAG GCT CAT GGG GTC CGA GTG Ser Asn Met Glu Arg Leu Leu His Ala Lys Ala His Gly Val Arg Val			768
240	245	250	
ATT GGC AGC TCC ACC TTG GCG CTC TGC TAC TTG GCC TCG GGG GCT GCT Ile Gly Ser Ser Thr Leu Ala Leu Cys Tyr Leu Ala Ser Gly Ala Ala			816
255	260	265	270
GAT GCC TAT TAC CAG TTC GGC CTC CAC TGC TGG GAT CTG GCA GCT GCC Asp Ala Tyr Tyr Gln Phe Gly Leu His Cys Trp Asp Leu Ala Ala Ala			864
275	280	285	
ACA GTC ATC ATC AGA GAA GCA GGT GGC ATT GTG ATT GAC ACC TCA GGT Thr Val Ile Ile Arg Glu Ala Gly Ile Val Ile Asp Thr Ser Gly			912
290	295	300	
GGA CCC CTT GAC CTC ATG TCG TGC AGA GTG GTG GCT GCT GGC ACC AGA Gly Pro Leu Asp Leu Met Ser Cys Arg Val Val Ala Ala Gly Thr Arg			960
305	310	315	
GAG ATG GCA GTG CTC ATA GCT CAG GCC CTA CAA ACC ATT AAC TAC GGC Glu Met Ala Val Leu Ile Ala Gln Ala Leu Gln Thr Ile Asn Tyr Gly			1008
320	325	330	
CGG GAC GAT GAG AAG TGAGCCGTAC AGAGCTCTAA GGCTGACATG AGCAGCTCCC Arg Asp Asp Glu Lys			1063
335			
TGGGAAAGAG CTGTCCGGGG GCTTGAGTTC CGGGATAGTC TACCATAGCT GTCCCCGGAC			1123
CTCGGTGCTT AGCTGATCCT CTCTAACCTC GGGTAGCCCC TTTCCAGGTC GGTACATGGT			1183
CTTTCATCAG AGCCAAACCC AAATCTTGTG AGGTGTGTTA GTCACCCATC CTGGTTGTT			1243
GGAATGCAA TCTCAGGTAA TAAAGCTTTA GAACGAGCTC TCAGGCCCTC CCCTGCCGT			1303
GGTGATACAG AATGCAATAA ATCAGAACTT TAAAAAA			1339

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Gly Ala Leu Glu Asp Ala Arg Leu Gly Gly Lys Ala Arg Gly Pro Cys
1 5 10 15

Gly Ala Ser Gly Ala Gly Gly His Gln Phe Gly Ser Arg Glu Pro
20 25 30

Ala Ala Ala Arg Gly Thr Glu Gln Arg Val Ala Gly Pro Gly Glu Thr

35	40	45
Thr Met Lys Pro Asn Ser Glu	Glu Glu Glu	Leu Val Gln Gly Val
50	55	60
Gly Pro Trp Asp Glu Cys	Phe Glu Val Ala Val	Gln Leu Ala Leu Arg
65	70	75
Ala Gly Gln Ile Ile Arg Lys Ala Leu	Thr Glu Glu Lys His Val Ser	
85	90	95
Thr Lys Thr Ser Ala Ala Asp Leu Val	Thr Glu Thr Asp His Arg Val	
100	105	110
Glu Asp Leu Ile Val Ser Glu	Leu Arg Lys Arg Phe Pro Ser His Arg	
115	120	125
Phe Ile Ala Glu Glu Ala Thr Ala Ser Gly Ala Lys	Cys Val Leu Thr	
130	135	140
His Ser Pro Thr Trp Ile Ile Asp Pro Ile Asp Gly	Thr Cys Asn Phe	
145	150	155
Val His Arg Phe Pro Thr Val Ala Val Ser Ile Gly	Phe Ala Val His	
165	170	175
Gln Glu Leu Glu Phe Gly Val Ile His His Cys Thr	Glu Glu Arg Leu	
180	185	190
Tyr Thr Gly Arg Arg Gly Gln Gly Ala Phe Cys Asn	Gly Gln Arg Leu	
195	200	205
Gln Val Ser Arg Glu Thr Asp Leu Ala Lys Ala	Leu Val Thr Glu	
210	215	220
Ile Gly Pro Lys Arg Asp Pro Asp Thr Leu Lys Val	Phe Leu Ser Asn	
225	230	235
Met Glu Arg Leu Leu His Ala Lys Ala His	Gly Val Arg Val Ile Gly	
245	250	255
Ser Ser Thr Leu Ala Leu Cys Tyr Leu Ala Ser Gly	Ala Ala Asp Ala	
260	265	270
Tyr Tyr Gln Phe Gly Leu His Cys Trp Asp Leu Ala	Ala Ala Thr Val	
275	280	285
Ile Ile Arg Glu Ala Gly Gly	Ile Val Ile Asp Thr Ser Gly Gly Pro	
290	295	300
Leu Asp Leu Met Ser Cys Arg Val Val Ala Ala	Gly Thr Arg Glu Met	
305	310	315
Ala Val Leu Ile Ala Gln Ala Leu Gln Thr Ile Asn	Tyr Gly Arg Asp	
325	330	335
Asp Glu Lys		

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2285 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HW059

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 9..1271

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION: 1991..2162
 (D) OTHER INFORMATION: /label= SAC_24457

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GTCGACAG CCC GCC ACT CCA GGC GCG ATG CTG TTC TGG ACT GTG CTC AGC	50
Pro Ala Thr Pro Gly Ala Met Leu Phe Trp Thr Val Leu Ser	
1 5 10	
ATG GCT TTG AGT CTG CGG TTG GCA CTG GCG CAG AGC GGC ATA GAG CGC	98
Met Ala Leu Ser Leu Arg Leu Ala Leu Ala Gln Ser Gly Ile Glu Arg	
15 20 25 30	
GGT CCC ACA GCA TCA GCC CCC CAG GGG GAC CTG TTG TTC CTG CTG GAC	146
Gly Pro Thr Ala Ser Ala Pro Gln Gly Asp Leu Leu Phe Leu Leu Asp	
35 40 45	
AGC TCA GCC AGT GTG TCA CAC TAT GAG TTC TCA AGA GTT CGA GAG TTT	194
Ser Ser Ala Ser Val Ser His Tyr Glu Phe Ser Arg Val Arg Glu Phe	
50 55 60	
GTG GGG CAG CTG GTG GCT ACG ATG CCT TTC GGA CCC GGG GCT CTG CGT	242
Val Gly Gln Leu Val Ala Thr Met Pro Phe Gly Pro Gly Ala Leu Arg	
65 70 75	
GCT AGT CTG GTG CAC GTG GGC AGC CGG CCT CAC ACG GAG TTT ACT TTT	290
Ala Ser Leu Val His Val Gly Ser Arg Pro His Thr Glu Phe Thr Phe	
80 85 90	
GAT CAG TAC AGT TCA GGC CAG GCC ATA CAG GAT GCT GTA CGT GTT GCG	338
Asp Gln Tyr Ser Ser Gly Gln Ala Ile Gln Asp Ala Val Arg Val Ala	
95 100 105 110	
CCC CAA CGT ATG GGT GAC ACC AAC ACG GGC CTG GCA CTG GCT TAT GCC	386
Pro Gln Arg Met Gly Asp Thr Asn Thr Gly Leu Ala Leu Ala Tyr Ala	
115 120 125	
AAA GAA CAA TTA TTT GCT GAG GAA GCA GGT GCC CGG CTA GGG GTT CCC	434
Lys Glu Gln Leu Phe Ala Glu Glu Ala Gly Ala Arg Leu Gly Val Pro	
130 135 140	
AAG GTA CTG GTG TGG GTG ACA GAT GGG GCC TCC AGT GAC TCT GTG GGC	482
Lys Val Leu Val Trp Val Thr Asp Gly Ala Ser Ser Asp Ser Val Gly	
145 150 155	

CCC CCT ATG CAG GAG CTC AAG GAC CTG GGT GTC ACC ATC TTC ATT GTC Pro Pro Met Gln Glu Leu Lys Asp Leu Gly Val Thr Ile Phe Ile Val 160 165 170	530
AGC ACT GGC CGA GGC AAC CTG TTG GAG CTG TTG GCA GCT GCC TCA GCT Ser Thr Gly Arg Gly Asn Leu Leu Glu Leu Leu Ala Ala Ser Ala 175 180 185 190	578
CCG GCT GAG AAG CAC CTA CAC TTT GTG GAT GTG GAT GAC CTT CCT ATC Pro Ala Glu Lys His Leu His Phe Val Asp Val Asp Asp Leu Pro Ile 195 200 205	626
ATT GCC CGG GAG CTT CGG GGT GCC ATT ATT GAT GCG ATG CAG CCA CAT Ile Ala Arg Glu Leu Arg Gly Ala Ile Ile Asp Ala Met Gln Pro His 210 215 220	674
CAG CTT CAT GCT TCG GAG ATT CTG TCC AAT GGC TTC CGC CTG TCC TGG Gln Leu His Ala Ser Glu Ile Leu Ser Asn Gly Phe Arg Leu Ser Trp 225 230 235	722
CCG CCC CTG CTG ACA GCG GAC TCT GGT TAC TAC GTG CTG GAG TTG GTG Pro Pro Leu Leu Thr Ala Asp Ser Gly Tyr Tyr Val Leu Glu Leu Val 240 245 250	770
CCC AGT GGC AAA CTG GCA GCC ACA AGA CGC CAA CAG CTG CCC GGG AAT Pro Ser Gly Lys Leu Ala Ala Thr Arg Arg Gln Gln Leu Pro Gly Asn 255 260 265 270	818
GCT ACC AGC TGG ACC TGG ACC GAC CTC AAC CCA GAC ACA GAT TAC GAA Ala Thr Ser Trp Thr Trp Thr Asp Leu Asn Pro Asp Thr Asp Tyr Glu 275 280 285	866
GTA TCG CTG TTG CCG GAG TCC AAT GTG CGC CTC CTG AGG CCC CAG CAC Val Ser Leu Leu Pro Glu Ser Asn Val Arg Leu Leu Arg Pro Gln His 290 295 300	914
TTG CGA GTA CGC ACA CTG CAA GAG GAG GCA GGG CCA GAA CGC ATC GTC Leu Arg Val Arg Thr Leu Gln Glu Ala Gly Pro Glu Arg Ile Val 305 310 315	962
ATC TCG CAT ACT AGG CCG CGC AGC CTC CGT GTA AGT TGG GCC CCC GCA Ile Ser His Thr Arg Pro Arg Ser Leu Arg Val Ser Trp Ala Pro Ala 320 325 330	1010
CTT GGC CCG GAC TCC ACT CTC GGC TAC CTT GTA CAG CTC GGA CCT CTG Leu Gly Pro Asp Ser Thr Leu Gly Tyr Leu Val Gln Leu Gly Pro Leu 335 340 345 350	1058
CAG GGC GGA TCC CTA GAA CAC GTG GAG GTG CCA GCT GGC CAG AAC AGC Gln Gly Ser Leu Glu His Val Glu Val Pro Ala Gly Gln Asn Ser 355 360 365	1106
ACT ACC ATC CAG GGC CTG ACG CCC TGC ACC ACT TAC CTG GTG ACT GTG Thr Thr Ile Gln Gly Leu Thr Pro Cys Thr Thr Tyr Leu Val Thr Val 370 375 380	1154
ACT GCC GCC TTC CGC TCG GGC CGC CAG AGG GCG CTG TCG GCT AAG GCC Thr Ala Ala Phe Arg Ser Gly Arg Gln Arg Ala Leu Ser Ala Lys Ala 385 390 395	1202
TGT ACG GCA TCT GGC GAG CGG ATC CGT GTC CCG CAG GCC ATG CGG CCG Cys Thr Ala Ser Gly Glu Arg Ile Arg Val Pro Gln Ala Met Arg Pro	1250

400	405	410		
GAG	GCC	GGA	CTG CGG GAG CCC TGACCTTCCT GCCTCGTCCA CCCGAGGGGC Glu Ala Gly Leu Arg Glu Pro	1301
415		420		
CCTCTTCCCT	AATCCAGTGA	GAGAGGCACC	GCTGCTCGTG GTTTTCTTG TGGATGGAGT	1361
GGGGTGGGGA	GATGGGGGTG	CTGGTCCTAC	CTTGACCTG CGTAACTCCT CCGGTCGTT	1421
CCCCACTGGT	CATCACCGCC	CTTGCTGAC	TCCCAGGAAA CCTGTAGCAA CCCTGGTAGC	1481
CTCACCGCA	ATGACAATCC	TCTCCGGTTG	CCAGTGGAGT TGAGCACACG GTGGTCCTTG	1541
GGCAACATTT	GGCGAGGGGA	TGGACAGTGT	TTGAGGTCAAG GTTGAGACCC AGGAGAAGCA	1601
TTCAGGAGAG	GAGGCCACAG	AGTTTTCTAC	CTGTGCCAAA GACTGGGCC TCTGGTGGCA	1661
AGGACTACAC	ATGGCTTGGA	GGAAATGTCC	AGGACCCCTTC AAGTCCTGCC TGTGCCTAGA	1721
AAGTGGGTAG	GAGAAAGGGA	GGAGAGAGTA	GTGTAGGCAA GGTTCCCAA GACTTCCTTA	1781
GGGCAAGGAA	AGGTAGGGAG	AGATAACCGGG	AGGCTGATGA TGTTGCCAAC TAGTTTCAT	1841
CAAGATTTC	TGCCAGCCTG	GAGGCCAGGA	TCTGTCAAGGG TCACTGACTC TGCCCTTCCTG	1901
CCCAGGACCT	GCAC TGGGCC	CCGCTATCAG	TGCGGGGGGG GGGGTGCAGA GTCTTCACAG	1961
GAATGGGGGA	TGAGACCTTG	GCATGTAGTA	CATTGGGGAT AGGAGAGCCC TGCCGTGACA	2021
GACTTACAGG	GAGTCTCCTG	CTTTAGTGTG	GGGAGCAAGG TGACATGCAG GTGGGCTACC	2081
TCCTGTCATC	ACTACTGCC	TGGGGCATCT	GACAGATACC TAAGGGTAGT CAGGAACAGG	2141
CTTCCTCTCC	AGTCCCTATG	TACGCAGAGC	CCCTCCTCCC CAGAACCTCT TGCCCTAACCC	2201
TAAGCTTACT	CCATCTCTCT	TCCCCACTAA	TGACCCAGAC TCTAACAAATA ATACAGTAAG	2261
CCAGATGTAA	ACTGTGAAGT	CGAC		2285

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 421 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Pro	Ala	Thr	Pro	Gly	Ala	Met	Leu	Phe	Trp	Thr	Val	Leu	Ser	Met	Ala
1						5				10				15	
Leu	Ser	Leu	Arg	Leu	Ala	Leu	Ala	Gln	Ser	Gly	Ile	Glu	Arg	Gly	Pro
										20	25		30		
Thr	Ala	Ser	Ala	Pro	Gln	Gly	Asp	Leu	Leu	Phe	Leu	Leu	Asp	Ser	Ser
										35		40	45		
Ala	Ser	Val	Ser	His	Tyr	Glu	Phe	Ser	Arg	Val	Arg	Glu	Phe	Val	Gly
										50	55	60			

Gln Leu Val Ala Thr Met Pro Phe Gly Pro Gly Ala Leu Arg Ala Ser
 65 70 75 80
 Leu Val His Val Gly Ser Arg Pro His Thr Glu Phe Thr Phe Asp Gln
 85 90 95
 Tyr Ser Ser Gly Gln Ala Ile Gln Asp Ala Val Arg Val Ala Pro Gln
 100 105 110
 Arg Met Gly Asp Thr Asn Thr Gly Leu Ala Leu Ala Tyr Ala Lys Glu
 115 120 125
 Gln Leu Phe Ala Glu Glu Ala Gly Ala Arg Leu Gly Val Pro Lys Val
 130 135 140
 Leu Val Trp Val Thr Asp Gly Ala Ser Ser Asp Ser Val Gly Pro Pro
 145 150 155 160
 Met Gln Glu Leu Lys Asp Leu Gly Val Thr Ile Phe Ile Val Ser Thr
 165 170 175
 Gly Arg Gly Asn Leu Leu Glu Leu Ala Ala Ala Ser Ala Pro Ala
 180 185 190
 Glu Lys His Leu His Phe Val Asp Val Asp Asp Leu Pro Ile Ile Ala
 195 200 205
 Arg Glu Leu Arg Gly Ala Ile Ile Asp Ala Met Gln Pro His Gln Leu
 210 215 220
 His Ala Ser Glu Ile Leu Ser Asn Gly Phe Arg Leu Ser Trp Pro Pro
 225 230 235 240
 Leu Leu Thr Ala Asp Ser Gly Tyr Tyr Val Leu Glu Leu Val Pro Ser
 245 250 255
 Gly Lys Leu Ala Ala Thr Arg Arg Gln Gln Leu Pro Gly Asn Ala Thr
 260 265 270
 Ser Trp Thr Trp Thr Asp Leu Asn Pro Asp Thr Asp Tyr Glu Val Ser
 275 280 285
 Leu Leu Pro Glu Ser Asn Val Arg Leu Leu Arg Pro Gln His Leu Arg
 290 295 300
 Val Arg Thr Leu Gln Glu Glu Ala Gly Pro Glu Arg Ile Val Ile Ser
 305 310 315 320
 His Thr Arg Pro Arg Ser Leu Arg Val Ser Trp Ala Pro Ala Leu Gly
 325 330 335
 Pro Asp Ser Thr Leu Gly Tyr Leu Val Gln Leu Gly Pro Leu Gln Gly
 340 345 350
 Gly Ser Leu Glu His Val Glu Val Pro Ala Gly Gln Asn Ser Thr Thr
 355 360 365
 Ile Gln Gly Leu Thr Pro Cys Thr Thr Tyr Leu Val Thr Val Thr Ala
 370 375 380
 Ala Phe Arg Ser Gly Arg Gln Arg Ala Leu Ser Ala Lys Ala Cys Thr
 385 390 395 400

Ala Ser Gly Glu Arg Ile Arg Val Pro Gln Ala Met Arg Pro Glu Ala
 405 410 415

Gly Leu Arg Glu Pro
 420

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2521 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HW061

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..1422

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: complement (2089..2287)
- (D) OTHER INFORMATION: /label= SAC_24029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GTGCGAC GCG ACG GTG GCG GAG CAG TGG GTG CTG GTG GAG ATG GTG CAG	48
Ala Thr Val Ala Glu Gln Trp Val Leu Val Glu Met Val Gln	
1 5 10	
GCG CTG TAC GAG GCT CCA GCA TAC CAT CTA ATT CTG GAA GGA ATC CTC	96
Ala Leu Tyr Glu Ala Pro Ala Tyr His Leu Ile Leu Glu Gly Ile Leu	
15 20 25 30	
ATA CTT TGG ATA ATC AGA CTC GTT TTC TCT AAA ACT TAC AAG TTG CAG	144
Ile Leu Trp Ile Ile Arg Leu Val Phe Ser Lys Thr Tyr Lys Leu Gln	
35 40 45	
GAG CGT TCT GAC CTT ACA GCC AAG GAA AAG GAA GAA CTG ATT GAA GAA	192
Glu Arg Ser Asp Leu Thr Ala Lys Glu Lys Glu Glu Leu Ile Glu Glu	
50 55 60	
TGG CAG CCA GAG CCC CTC GTC CCC CCG GTC TCC AGG AAC CAT CCT GCT	240
Trp Gln Pro Glu Pro Leu Val Pro Pro Val Ser Arg Asn His Pro Ala	
65 70 75	
CTC AAC TAC AAC ATC GTC TCC GGC CCT CCA ACC CAT AAC ATC GTG GTG	288
Leu Asn Tyr Asn Ile Val Ser Gly Pro Pro Thr His Asn Ile Val Val	
80 85 90	
AAC GGA AAA GAG TGT GTC AAC TTT GCC TCC TTT AAT TTC CTC GGG TTG	336
Asn Gly Lys Glu Cys Val Asn Phe Ala Ser Phe Asn Phe Leu Gly Leu	
95 100 105 110	

CTG GCC AAC CCT CGG GTT AAG GCT GCG GCT TTT GCA TCA TTA AAG AAG Leu Ala Asn Pro Arg Val Lys Ala Ala Phe Ala Ser Leu Lys Lys 115 120 125	384
TAT GGC GTG GGT ACC TGT GGT CCC AGA GGG TTT TAT GGC ACA TTT GAT Tyr Gly Val Gly Thr Cys Gly Pro Arg Gly Phe Tyr Gly Thr Phe Asp 130 135 140	432
GTC CAT CTG GAT TTG GAA GAG CGC CTG GCA AAG TTT ATG AAG ACC GAA Val His Leu Asp Leu Glu Arg Leu Ala Lys Phe Met Lys Thr Glu 145 150 155	480
GAA GCT ATC ATT TAC TCC TAT GGC TTC TCC ACC ATA GCC AGT GCG ATT Glu Ala Ile Ile Tyr Ser Tyr Gly Phe Ser Thr Ile Ala Ser Ala Ile 160 165 170	528
CCT GCG TAC TCT AAG AGA GGG GAC ATT GTT TTT GTG GAC AGT GCA GCC Pro Ala Tyr Ser Lys Arg Gly Asp Ile Val Phe Val Asp Ser Ala Ala 175 180 185 190	576
TGC TTT GCT ATC CAG AAA GGA CTA CAG GCA TCA CGC AGT GAC ATT AAG Cys Phe Ala Ile Gln Lys Gly Leu Gln Ala Ser Arg Ser Asp Ile Lys 195 200 205	624
TTA TTC AAG CAC AAT GAC GTA GCT GAC CTG GAG CGA CTG CTA AAA GAA Leu Phe Lys His Asn Asp Val Ala Asp Leu Glu Arg Leu Leu Lys Glu 210 215 220	672
CAA GAG ATT GAA GAT CAA AAG AAT CCT CGA AAG GCC CGT GTG ACT CGG Gln Glu Ile Glu Asp Gln Lys Asn Pro Arg Lys Ala Arg Val Thr Arg 225 230 235	720
CGA TTC ATC GTC GCG GAA GGA TTG TAT ATG AAC ACT GGA ACC ATC TGC Arg Phe Ile Val Ala Glu Gly Leu Tyr Met Asn Thr Gly Thr Ile Cys 240 245 250	768
CCT CTT CCA GAA CTG GTG AGG TTA AAG TAT AAA TAC AAA GCA AGG ATC Pro Leu Pro Glu Leu Val Arg Leu Lys Tyr Lys Tyr Lys Ala Arg Ile 255 260 265 270	816
TTC CTG GAG GAG AGC CTG TCG TTC GGA GTC CTT GGG GAG CAT GGG CGA Phe Leu Glu Glu Ser Leu Ser Phe Gly Val Leu Gly Glu His Gly Arg 275 280 285	864
GGA GTC ACC GAG CAC TAT GGG ATC AGT ATT GAC GAC ATC GAC CTT ATC Gly Val Thr Glu His Tyr Gly Ile Ser Ile Asp Asp Ile Asp Leu Ile 290 295 300	912
AGT GCT AAC ATG GAG AAT GCG CTC GCT TCT GTT GGG GGC TTC TGC TGT Ser Ala Asn Met Glu Asn Ala Leu Ala Ser Val Gly Gly Phe Cys Cys 305 310 315	960
GGC CGC TCT TTC GTG GTT GAC CAT CAG CGG CTC TCT GGC CAA GGA TAC Gly Arg Ser Phe Val Val Asp His Gln Arg Leu Ser Gly Gln Gly Tyr 320 325 330	1008
TGC TTT TCA GCT TCA CTG CCC CCC CTG CTA GCC GCT GCC GCC ATT GAG Cys Phe Ser Ala Ser Leu Pro Pro Leu Leu Ala Ala Ala Ile Glu 335 340 345 350	1056
GCC CTC AAC ATC ATG GAG GAG AAC CCA GGG ATT TTT GCA GTT TTA AAG Ala Leu Asn Ile Met Glu Glu Asn Pro Gly Ile Phe Ala Val Leu Lys 355 360 365	1104

AAA AAG TGC CAG ACC ATC CAC AAG TCC CTA CAA GGG GTT TCC GGT TTA Lys Lys Cys Gln Thr Ile His Lys Ser Leu Gln Gly Val Ser Gly Leu 370 375 380	1152
AAA GTG GTG GGG GAG TCC CTT TGC CCA GCG CTT CAC CTC CAG CTG GAA Lys Val Val Gly Glu Ser Leu Cys Pro Ala Leu His Leu Gln Leu Glu 385 390 395	1200
GAG AGC ACG GGC TCT CGG GAG AGA GAT ATG AAG CTG CTT CAG GAG ATT Glu Ser Thr Gly Ser Arg Glu Arg Asp Met Lys Leu Leu Gln Glu Ile 400 405 410	1248
GTA GAG CAA TGC ATG AAT AAG GGC ATC GCA TTG ACT CAG GCA CGC TAC Val Glu Gln Cys Met Asn Lys Gly Ile Ala Leu Thr Gln Ala Arg Tyr 415 420 425 430	1296
TTG GAC AAG GAA GAG AAG TGC CTT CCT CCT CCA AGC ATC AGG GTT GTG Leu Asp Lys Glu Glu Lys Cys Leu Pro Pro Ser Ile Arg Val Val 435 440 445	1344
GTC ACC GTG GAG CAG ACA GAC GAA GAG CTG CAG AGG GCT GCA GCC ACC Val Thr Val Glu Gln Thr Asp Glu Glu Leu Gln Arg Ala Ala Ala Thr 450 455 460	1392
ATC AGG GAG GCG GCC CAG GCT GTG CTT TTG TAGGCTCCTG CCCAGTGCTT Ile Arg Glu Ala Ala Gln Ala Val Leu Leu 465 470	1442
GCGACCATGT CACCTGCAGA CAGAACTACT CAGACCTCCA GCTGCCAGG GCGTGGAGTG	1502
CTGCCAGGG CGTGGCTGCC CTTGAGTCCA CAGCCAGAAT GGATGGCTTT ACCCAGCAGG	1562
CTTCCAGAGG ATGGCAGACG ACGGTGTAAC ACTGGTGT TTGATGGCTGCC ATGGCTCTGT	1622
CTCTTATACT CGCCTTGTT TAAAACTGGA GCTTCCGTTT TCCCTCTCCC GCCTGTGGGA	1682
ACAATTGAT AACCACTCCT CTGTATTCCA TACAAAAGGA CTGAGCTG AGAGGAAGTC	1742
TCCACGCACC ACAGTTACTG TGGGATGATA GACTGTGCC TCCCAGGTCC TTCGGGTAGA	1802
GCTCAGTGGT GGCTGCTGTG CAGACAACTC CTGTGTGTCA AAACATGTCAT AGAACATGTT	1862
GATCCTAGAA CTCTGTGTGC TCCAGTTACT GATGCTGTG TGCTAAATCT GAGCTTCACT	1922
AACAATAGTC ATACCGCTCC CTAAGCAATA ATCTGAATCA AACATTATTT TATTTTTGTG	1982
TAATTGACTT TATATTTTTT ATATATTCTC TAGTCAGTTT TGGGAAGAGGG GTTATTATTC	2042
TGGTCCCCAA ATATATAAAT CATATCCTTG GTATTTTTA ATATGTACGG TGTCCTTTT	2102
CATGGTGGTT TTGTCAGGA ACATAGAACT GTGGGCCCTT TCTAAGCTGA GAAAAGAGAG	2162
AACTTTCTTC TTTCGTTCTA TAAATTCCAG ATGCCCTCAGA AAATAGGAAT GCTCTGAAA	2222
CTGCTGCTGT CCTTAGCGAG CGTGCTGAGG GGTGTAACGG CTTGTGACAT GTGCCGCGAT	2282
CGTGTACATG GAAGGCCATT ACTCCCTCTC GCTGCACAGG CAGAGGAATG GGGCCTCTAA	2342
CCGTCGTTT CGGATGTTCA TTCATGTTAA CAGTGGACGG CATCTTCCTA AGTGATCTGT	2402
GACATGTTA ATGTGTCTAT TTCATACGTG CCTTGTGAAT GCTGCTGCTG TGAGGGTACG	2462

GGGATGAGTC TGTGTTGGTT TGTTTTAA TGAAATAAAC CTCCAAGAGC CTACAAAAA 2521

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 472 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Ala Thr Val Ala Glu Gln Trp Val Leu Val Glu Met Val Gln Ala Leu
 1 5 10 15

Tyr Glu Ala Pro Ala Tyr His Leu Ile Leu Glu Gly Ile Leu Ile Leu
 20 25 30

Trp Ile Ile Arg Leu Val Phe Ser Lys Thr Tyr Lys Leu Gln Glu Arg
 35 40 45

Ser Asp Leu Thr Ala Lys Glu Lys Glu Glu Leu Ile Glu Glu Trp Gln
 50 55 60

Pro Glu Pro Leu Val Pro Pro Val Ser Arg Asn His Pro Ala Leu Asn
 65 70 75 80

Tyr Asn Ile Val Ser Gly Pro Pro Thr His Asn Ile Val Val Asn Gly
 85 90 95

Lys Glu Cys Val Asn Phe Ala Ser Phe Asn Phe Leu Gly Leu Leu Ala
 100 105 110

Asn Pro Arg Val Lys Ala Ala Ala Phe Ala Ser Leu Lys Lys Tyr Gly
 115 120 125

Val Gly Thr Cys Gly Pro Arg Gly Phe Tyr Gly Thr Phe Asp Val His
 130 135 140

Leu Asp Leu Glu Glu Arg Leu Ala Lys Phe Met Lys Thr Glu Glu Ala
 145 150 155 160

Ile Ile Tyr Ser Tyr Gly Phe Ser Thr Ile Ala Ser Ala Ile Pro Ala
 165 170 175

Tyr Ser Lys Arg Gly Asp Ile Val Phe Val Asp Ser Ala Ala Cys Phe
 180 185 190

Ala Ile Gln Lys Gly Leu Gln Ala Ser Arg Ser Asp Ile Lys Leu Phe
 195 200 205

Lys His Asn Asp Val Ala Asp Leu Glu Arg Leu Leu Lys Glu Gln Glu
 210 215 220

Ile Glu Asp Gln Lys Asn Pro Arg Lys Ala Arg Val Thr Arg Arg Phe
 225 230 235 240

Ile Val Ala Glu Gly Leu Tyr Met Asn Thr Gly Thr Ile Cys Pro Leu
 245 250 255

Pro Glu Leu Val Arg Leu Lys Tyr Lys Tyr Lys Ala Arg Ile Phe Leu

260	265	270	
Glu Glu Ser Leu Ser Phe Gly Val Leu Gly Glu His Gly Arg Gly Val			
275	280	285	
Thr Glu His Tyr Gly Ile Ser Ile Asp Asp Ile Asp Leu Ile Ser Ala			
290	295	300	
Asn Met Glu Asn Ala Leu Ala Ser Val Gly Gly Phe Cys Cys Gly Arg			
305	310	315	320
Ser Phe Val Val Asp His Gln Arg Leu Ser Gly Gln Gly Tyr Cys Phe			
325	330	335	
Ser Ala Ser Leu Pro Pro Leu Leu Ala Ala Ala Ala Ile Glu Ala Leu			
340	345	350	
Asn Ile Met Glu Glu Asn Pro Gly Ile Phe Ala Val Leu Lys Lys Lys			
355	360	365	
Cys Gln Thr Ile His Lys Ser Leu Gln Gly Val Ser Gly Leu Lys Val			
370	375	380	
Val Gly Glu Ser Leu Cys Pro Ala Leu His Leu Gln Leu Glu Glu Ser			
385	390	395	400
Thr Gly Ser Arg Glu Arg Asp Met Lys Leu Leu Gln Glu Ile Val Glu			
405	410	415	
Gln Cys Met Asn Lys Gly Ile Ala Leu Thr Gln Ala Arg Tyr Leu Asp			
420	425	430	
Lys Glu Glu Lys Cys Leu Pro Pro Pro Ser Ile Arg Val Val Val Thr			
435	440	445	
Val Glu Gln Thr Asp Glu Glu Leu Gln Arg Ala Ala Ala Thr Ile Arg			
450	455	460	
Glu Ala Ala Gln Ala Val Leu Leu			
465	470		

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 598 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: HW062
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: complement (87..223)
 - (D) OTHER INFORMATION: /label= SAC_24443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TTTTGTGAG CAAATCCAAA TTTATTTAA TGCCATGTCA TTTCAAAAAC CCCAGCCTTG	60
GTTCCCTGGA ACAGCATGCC AGAGGTACAA AGTGTAACTT TCCTCTATAA ACCCCCAGCA	120
AGTCATCCAA GTCCTCAGCT TCAGAAAGTC AGTTCTCTTC AGTCTACTCC TCTGGTCCT	180
GGTTTTCTT TCAAGGAAGG CAACTAAAAA ATTAGGTAGC TGAGGTTCCA ATGTTGGTGG	240
CTAACCTTGC CTCCTCTTT GTTCTGTAGT AGGGCCACAA ACCTTGACCA GGCAGAGTAG	300
TAGAAAAGTA GAAAGAGGGG CTTGACGACG GTGGATTTCG ACTCCTGATT TTATTATTCA	360
ATTTCTTTT CTACTAAAAG TAGTCTCGG TGGTTGGAA GCCTGGCCTC CCAACACCAG	420
AGTCAGTCGG AGCTGGTTTT TTTGTTGAAA GGAGTGGCG GGTGGGTGGG GGACCGGGAT	480
GAGGGCAGAA CCCCCTCTG CTGGTAGTCT TGGGTGGAGA AGACGAAC TG CACTTGACAG	540
AGCCTGGGGG TGCGGTGGGA GGGGGTGAGG CAGGAGTGAC AGCTGGGGAG GGGACCCA	598

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HW066

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 759..906
- (D) OTHER INFORMATION: /label= SAC_24521

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATTCGCGGCC GGCTCGACTT TTTTTTTTGT GATATAAAAA ATTATTTTA GAAATCACAT	60
CTTTAAAAAA CAACATAGAA GGTTATCCTG ACCAGATATA AATTCTTCAT TCAATGCCAG	120
GGTGTATGT GGTACAATTA CGGGGATGTT CTGTGAGGAG AATGAGTCTG TGTGATACTC	180
TCGACATGTA CACCAAGCTCA AACGTTAATG CGGCTTTAA AAGGAAGGAG AGAGGAAGGC	240
ACCGAGAGAG GAGGAAACTG TTTTGGAAAC AGAAGAGCAT CTCCGTCCCTG CACCTGTCAG	300
CCCTGAAACT CCCGGCCCTT GAGACCAGCC CAGCAGAGGC TGACGAANN NGCATCATT	360
TAATTACCAA GTGACTGCAG CACCCCTGGCA TCTTGTGCTG GGAGTGTGGG TGGGAACAGA	420

GGTGACAAGT CTGCTCTGTA GTGTCA TAGC CAGAGAGCAA CAGGGACTCT AGAGGAAGAA	480
GAGCAAAGCT TGCCTAGACA GAACGGGTTG TCCCTGTCCC TGTCCATCAG CTTTCTTATA	540
ACCTATGGNT AGCCAGGATC AAATACCTGA AAGTCAGAAT GTAAAATAAA AGTGTCA GATT	600
AACACTTATT GC GGACAGAA ATACAGCTCT TTACGCCAAC ACCATAAAC CCAGTGGTGA	660
GGCTGGGACA GACCCTTTAT GCCGAAGTTTC TCACAAC TCG GGACTGACTT ACTGGGGCCT	720
GGTCACTGCT TAATTGGTGA CCTCACACCA TTTCAGGTAC TTCTGCCAG CTCCTGATT	780
CTCTTCAGGA GAAACAGGAA GCAGACTTTG TTAGTAAGTG GGTCA TGCA GGCTGGGCCG	840
CCTACATGGG ACTTAACACA GAGAGAATAC TGCCAGCTTC CCAAACACTT CAAGAGAGAA	900
AAATGTCCAG AC GTGGGTGC TGCAGCAACC TTCCAAGAGT GAGGCCCTG CACCCCTCCTG	960
CACCCCTCGGC TGGGGACAGT GGGCTCTGGT GGCTTGAAC GAGTAGATCG GATCATTCCC	1020
TCCCTTTCT GAGACAAGGC TTCACTGTGT AGCCCNNGCT GCCCTGGAGC TCACTATT	1080
GACCAGGCTA GGATCTCACA GAGAACCAAC TGCCTCTGGC CTCTCAAGAG CTGGGATTAA	1140
GGTGTAAAAA GGGGGCTAAT GTAGCCCAGG CTGGCTCCTG CTCCACAGGG CTTGCAGGCC	1200
AGTTCTGGAT CCTACCAAGCA AGTACAAGCT GGTACCCAGA GGACGCTGCA GGATGGAAGG	1260
ACGGAAAGGCC AGGAGCCTTC GTTTGATTG ACGGGAAGGA GGAGGAACAG TGAGGTTGTG	1320
CATCTGAGCT TTATTACCAAG GACGATGATG TCACCTCAGG AAGGGACTGG GATCCCTGCA	1380
AGTGGTTCCA CATGGGACCC AGGTCCCTAG AGATGTGGCC CTCCTTGTGT GCCAAATGC	1440
ATCTGGAAAG AAAATACAGA AGGGGAGGGAG CAGCATAGGA GGAGACAAGT GTGACCCGAG	1500
GCCCCAGGAAG TACTTCCATA TTCTGCTCTT CTCCAGGCAC GAGAGTTGAA GGCGTGC	1560
AGCCCTGCAC TCGCTAAGCT GGTGAAGACC ACACCAAAAT CACTGTGACA GGACAGCTGC	1620
ACAGATCTGT TTCCGACTTT TCCCACCAAG ATTCTACACC AAGGTAAAAA AGAGCTTCCA	1680
CCACAAATCC AAGGCAGGAG CTGGGCGGCC ACACACCCGC CACAGATGGT GCAAGTTGCT	1740
CACTTCCGCA GCCGGTGGCA GGACAGGGAG GAGGGCAGAG TCCTGAGACA AGAACCCAG	1800
AGCGGGGCCA GTTCAGTCAG TGGTGGACCT CCGGTACCAAG AACCGAGCTC GGAAGTCGTC	1860
GCTGCACGTC ATGAAGCCAG GGTTGGTCGG GGAGTGCAC TGCAGCGCA CAATGTTGTT	1920
GTGGCCCAAGG GACAGCAGGT TCCCTGCGTC AGCTGCTCTA GAGTCCCAGC AGCACAGGCT	1980
GATGGTCCTT TCGTCCGGCA GCAAATATA GTCCCTCAGTG TGGTTGAACA CAGCCTGTGT	2040
CCGGGTGCAC TTGCCGTCCA CTCAGCCCTG CGCCTGTGTA CCTCACCAAGT GTCCCGTCCG	2100
TGGATATTTC CCCAGAGTTT AGCTACAGAG TCTTTYCCNN GAGTTTAGGC CTACAGAGTC	2160
TTTTCCACTT GAGAGGATGT ACTTGGAATT CTTGGAGAAA ATGGCAGAAC AGACTTCTGC	2220
CCCGTCGTGA GCTTTCTCAA AGGTTGTGAT GCAGCGATTG GAGACGCCGT CCCACAGCTT	2280

GATGCAGCCG TCCTTGCTGC CAGTGACATA CATGTTGGCA CTAGGGTTAT AGTTGACAGA	2340
GCAGATGGCG TCGGTGTGCT GGTCTTGGGG ATTGCAGGAG ACGAAACACT GGAAGGTGTT	2400
GATGTCATAG AGGCCAAGCG TGGGATGCTG GGTCCCGACC AGGATGAAGT CTCCAGAAGG	2460
GTGGAACGAG ATGGAGCGCA GCATCTCAGC TTCCCTGAATG TATTTAAAGG CTCTTTTGC	2520
AGAGGGTTTG GAATAATCAA ACAATTAG AGTATAATCC CTTGAGCCGG AGGCCAGGAT	2580
CTGTTCTGTT GGGTGAAAAG CGAGACACGT GACTTCATCC ACATGGTCGT AAAGAGTCG	2640
GATCACTGGG TGGTTCTCCA TGTTCTGTTG TGCAGTCTCA TTCATCATGA CCCTCGATGG	2700
GCATGGCGCT CTTGGCCAGC ATCCCTCTG TGTCCAGTAT CTTGATGGAA GCATCCGCAG	2760
ACCCCTGTGGC TATCAACTGC CCATCTCTGC TGTAGGTGGC CACTCGGCAT GGGCCTTTGT	2820
GGGAGGTGAC ATAACAGGTT TCATACTCCG AAGCCTCGGG TGACATTGTT TGGACGTCTG	2880
CATCAAACTC CAGGTCAATN CTGTGCCAGG GGCAACCGTG TCAGAGCGAC CAATGGCATA	2940
CTGAAGTGCA GTGTCATCGT TCTCCATCCC TAGCTTGATG AGGTGCAGGA GCTGCTCCGA	3000
GGGCGCACAC ACCGACTGTG GCTTGATCTC GTTGATGAGG CCATTGCGAT GCTAATGTAT	3060
CCGTCATAGA GCAGCTGGCT GATGATCAGC TTGTAGAGCT GCTGGCGGTC CTTCAGGCC	3120
ACTTTGGTTC TGACATTCT GCACAAGAGG ATGACAGTTC CCCTGACTTC TCCGAGCTGA	3180
TCACCTCCGC GACAGCCTTG AATCAAAGG ACTGTGAGTG ACCGGCAAAC GCCCGANCCT	3240
TGGAGAGCAC NGCGGGCGAT AGAACGGCCG TAGATCGGAC AGGCCGTTGG TGCACCGTCG	3300
ACCGG	3305

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2099 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HW069

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1360..1893

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1744..1885
- (D) OTHER INFORMATION: /label= SAC_24477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GTCGACGCAT CCAGGCAGGC ATGGAGCAGG TAGGGCTCAG AGTTCTACAT CTTCATCTGG	60
AGGCTACTAT GAGGAGACCG ACTTCCAGGC AGCTAGGAAG CCCATGCTCA CAGTGACAGA	120
CCTTCTCCAA CAAGGTTATA CCTCCTAACAT GTGCCGCTCC CTGGGCAAG CATATGCAA	180
CCTTCACACA GGTCTTCCTC CTACACAGTG GGGCTCTGG GCCCCACTCA CGGCCAGTAC	240
ATGGCAAAAG ACATTAAGA TGCACTTGGG CAAGCTCAGG GCCCTGTTCT GCAGCCAGGT	300
ATCATGGATG GAGGAAGTCC TGACTGAAAC AAAAATGTCT GTCCGCATTG TCATCTTGA	360
GAGCCTGAAC AAACCCCGAA CACCTCTGAC CTGGCACAGG GACCCTGAGT CTGCCTGCCT	420
GGCACTCTGA ACTTGCTGGC TACTGGGCTG AAGTCTCAGG ATCGAGGTAC AAGGACAAAG	480
CCTGTTGGTA TTATGTAGAC AGGAGCCCCA GGGGGCTCAG AGCAGGGGTT TACCGTTACT	540
CTTGGTCCAG CGGGCACAGT GGTCTTCCT CAGTTTTGT TTTTGTGTTT TTGTTTTTT	600
GTTTTGTGTTT TTGTTTTTG TTTGTTGTT TGTTTGTTT TGTTTTTGG TGCTGTTGAC	660
CCTGCAGTCT GGACTGCCCT CTTGGCAAT ACATTTGAT GGAAACCAAC TTCTGTGTTC	720
CCAGATCGGC AGCCTCTCCA TGCGAGCAC CCCTGTTCTA GCTAACCCGG ACATGCTACA	780
CCCCGCCGT GGTTGGTTCA TCTCCCCACT CCCCGCCGTG TCTTAATAAC ACGGTGGATG	840
GATGGACAGA CGGACAGATG AAGCTTGAC AGCTAGCCAC TGCTCTGCTC CTTTTCTCTT	900
GTCTTCTGAG TAAATTCTCA AACTCAAGCC TCCCAGGGGG AGCCCAGAAC CCCACCCACC	960
ACTAGTAAA AAGCAGCTTT TTAGGCAGCT CAGAGAGTGT CCGGAGCAGG GTTCCTACAG	1020
GCTCAGGTTG GGGCAGTTT CAGTGTGTGG CTGCCGGCCC AGGGCCCTCC CTGGTCAGCA	1080
CCTAGGTAGA GAGGAAGCAG GAAGGACCAA GTCCAGCTCA AAGGAACCAG TGAGGCTGGT	1140
TGAGAGCAGA CGGTGGTAT GGGTCTGTGA AAAGAAAAGT AGGCCGTTGG GAGCCCACCG	1200
GAGGACAGTC TGGCTCAAGG CATCACACCT GGTTGCAGCA GCCTCCGAGA CAGCAGCCCG	1260
TGGGTGTGAA CTTGGCTCCA TCTTGGCTGA ATTCTGCTGC CCCAGAGAAC AATCTGGCAC	1320
CGGAGTGGAC CCAGATAACGT GTCACAGCCT TGGAAATCG ATG GCA GCG AGA CCC Met Ala Ala Arg Pro	1374
1 5	
TTT ATT GGG CAC CTA GAG ATT TCC GAG AGG CGG TTC CTA ACA TTG TCA Phe Ile Gly His Leu Glu Ile Ser Glu Arg Arg Phe Leu Thr Leu Ser	1422
10 15 20	
TTC CTT TCC CAC AGG CCT CAG GTC CAG GCC CAA AGC CAA GTG ACT GCC Phe Leu Ser His Arg Pro Gln Val Gln Ala Gln Ser Gln Val Thr Ala	1470
25 30 35	
CTC ATC GGC TCA GCA CAT CGG CGG GTG CTG GAT GTG CCG CCT GCA GAG Leu Ile Gly Ser Ala His Arg Arg Val Leu Asp Val Pro Pro Ala Glu	1518
40 45 50	
GCT CTT CGG GGC CAG GCT GGG ACT GGG CCC CTG AGA AAA CCC AAA CTC Ala Leu Arg Gly Gln Ala Gly Thr Gly Pro Leu Arg Lys Pro Lys Leu	1566

55	60	65	
TGT GCC TTA CCC AGT CAG GAT CCT TGG GAG CCT TGG CCC TCG ATG CCA Cys Ala Leu Pro Ser Gln Asp Pro Trp Glu Pro Trp Pro Ser Met Pro 70 75 80 85			1614
GGA CCT GGC CTA GCA TCA CCC TGG GCC ACC TGC ACG TTC ATG GCC TCA Gly Pro Gly Leu Ala Ser Pro Trp Ala Thr Cys Thr Phe Met Ala Ser 90 95 100			1662
CCA TCT GCT TTG CGA ACC ACT ACC CAC CCC CTG TCG CAT GCA CCT TCC Pro Ser Ala Leu Arg Thr Thr His Pro Leu Ser His Ala Pro Ser 105 110 115			1710
ACC CCT GCG GTG TCT GAC TCT AGG GAG ATA GGT ACA GAT GTC TGT GAT Thr Pro Ala Val Ser Asp Ser Arg Glu Ile Gly Thr Asp Val Cys Asp 120 125 130			1758
GGG CTG AGA CAT CCC CCA CCC CCC ACG GCT CAT TGG TTT CTT TTA GCT Gly Leu Arg His Pro Pro Pro Thr Ala His Trp Phe Leu Leu Ala 135 140 145			1806
GAG TGC TGT TTT CTG TGT CTT TAC TCT GCT ATG ATG ACT TGG GGG GTT Glu Cys Cys Phe Leu Cys Leu Tyr Ser Ala Met Met Thr Trp Gly Val 150 155 160 165			1854
AGT GAG GGC CTG AGG GAT GCT TGT TGG AAG TAC TGT GGG TAGGGCCTGG Ser Glu Gly Leu Arg Asp Ala Cys Trp Lys Tyr Cys Gly 170 175			1903
TAGGTCTTA GGGAACAAAC AAACAAAAGG CTCATCTGCT CCTGGGTGGT GACCTGGCCA			1963
CAGCACCTGT CATCTCCCTT GGTGTCTGCC CAGTGGGAC GAGCTTCCCT GGCTCAACCC			2023
CTATCAGGTG TGCACTGTTG AGTCTGCGGG CCAGCCGGGA CTTAACCAA TAAAGAGCAA			2083
CCTTGTCGTG CAAAAA			2099

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met Ala Ala Arg Pro Phe Ile Gly His Leu Glu Ile Ser Glu Arg Arg
1 5 10 15

Phe Leu Thr Leu Ser Phe Leu Ser His Arg Pro Gln Val Gln Ala Gln
20 25 30

Ser Gln Val Thr Ala Leu Ile Gly Ser Ala His Arg Arg Val Leu Asp
35 40 45

Val Pro Pro Ala Glu Ala Leu Arg Gly Gln Ala Gly Thr Gly Pro Leu
50 55 60

Arg Lys Pro Lys Leu Cys Ala Leu Pro Ser Gln Asp Pro Trp Glu Pro

65	70	75	80
Trp Pro Ser Met Pro Gly Pro Gly Leu Ala Ser Pro Trp Ala Thr Cys			
85		90	95
Thr Phe Met Ala Ser Pro Ser Ala Leu Arg Thr Thr His Pro Leu			
100		105	110
Ser His Ala Pro Ser Thr Pro Ala Val Ser Asp Ser Arg Glu Ile Gly			
115		120	125
Thr Asp Val Cys Asp Gly Leu Arg His Pro Pro Pro Pro Thr Ala His			
130		135	140
Trp Phe Leu Leu Ala Glu Cys Cys Phe Leu Cys Leu Tyr Ser Ala Met			
145		150	155
Met Thr Trp Gly Val Ser Glu Gly Leu Arg Asp Ala Cys Trp Lys Tyr			
165		170	175
Cys Gly			

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: HW070
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: complement (639..928)
 - (D) OTHER INFORMATION: /label= SAC_24286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GTCGACGCAG ATTTTGATGG CGTCCTTAT CATATTCAA ATCCTAATGG AGACAAAACA	60
AAAGTGTGATGG TCAGTATTTC TTTGAAATTC TACAAGGAAC TTCAGGCACA CGGAGCTGAT	120
GAGTTACTAA AGAGAGTATA CGGAAGTTTC TTGGTGAACC CAGAACTCAGG ATACAATGTG	180
TCTTTGCTAT ATGACCTGGA AAATCTACCT GCATCCAAGG ATTCTATTGT GCATCAGGCT	240
GGCATGTTGA AGCGAAATTG TTTTGCCTCT GTGTTGAGA AATACTTCCA ATTCCAAGAA	300
GAGGGCAAAG AAGGAGAGAA CAGAGCAGTT ATCCATTATA GAGATGATGA GACCATGTAT	360
GTGGAATCTA AAAAAGACAG AGTCACAGTA GTCTTCAGCA CAGTTTTAA GGATGACGAC	420

GATGTGGTCA TTGGAAAGGT GTTCATGCAG GAGTTCAAAG AAGGACGAAG AGCCAGCCAC	480
ACAGCCCCC AGGTCTTTT TAGCCACAGG GAACCTCCTC TAGAACTGAA AGACACAGAT	540
GCTGCCGTGG GTGACAACAT TGGCTACATC ACCTTGTGC TGTCCTCG CCACACCAAT	600
GCCACTGCTC GAGACAACAC CATCAACCTG ATCCACACGT TCCGGGACTA TCTGCACTAC	660
CACATTAAGT GCTCTAAGGC CTATATTCAT ACACGAATGC GAGCAAAAAC ATCCGACTTC	720
CTTAAGGTGC TCAACCGTGC ACGCCAGAT GCCGAGAAAA AAGAAATGAA AACAAATCACG	780
GGGAAGACTT TTTCATCCCG CTAACCTTG GGAACGTAGG AGGAAGCACT GTTGACCGAA	840
GGCTGGACCG CTTGCTACTG GATAATCGTA GCCCTTCATG TTGCACCTTC TCCAGGTTCT	900
TAAGGGATTC TCCGTTTGGG TTCCATTTG TACGAGTTG GCAAATACGC TGCAGAAACG	960
AGCTGTGCTT GCAAGGACTT GATAGTTCT AAGAATTAAA AACTCACTTG ATCAAATTAA	1020
TTCCCTTTA TTTTCCTCC CTCACTCCCC TTCCCTTTCC AAGCTGTTG CTTTGCAATA	1080
TGTTACTGGT AATGAGTTGC AGGTAATGCA ATCTTAACCTT GTTTCTTCT AAGTATTGAA	1140
GTTCAAAACT CCTGTATCTA AAGAAATACG GTTGGGGTCA TTAATAAAGA AAATCTTCT	1200
ATCTTAAAAA	1210

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1844 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HW073

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 9..1223

(xi) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 598..1036
 (D) OTHER INFORMATION: /label= SAC_24456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GTCGACCT GCC GGC CGA CAG GGC CGC GGG ATG AGG AAG CGG ACC GAG CCC	50
Ala Gly Arg Gln Gly Arg Gly Met Arg Lys Arg Thr Glu Pro	
1 5 10	
GTC ACC TTG GAG CAT GAG CGC TGC GCC TCA GGC TCG TCT TCC TCC	98
Val Thr Leu Glu His Glu Arg Cys Ala Ala Ser Gly Ser Ser Ser	
15 20 25 30	

GCC TCG GCC GCG GCG CTG GAC GCC GAC TGC AGC TTG AAG CAG AAC	146
Gly Ser Ala Ala Ala Leu Asp Ala Asp Cys Ser Leu Lys Gln Asn	
35 40 45	
CTG CGT CTG GCG AAG GGG ACG GCA GAG CCG CAC AGC GCA TCC GAC	194
Leu Arg Leu Ala Gly Lys Gly Thr Ala Glu Pro His Ser Ala Ser Asp	
50 55 60	
GCG GGC ATG AAG CGG GCT CTG GGC AGA CGG AAG AGC CTG TGG TTC CGA	242
Ala Gly Met Lys Arg Ala Leu Gly Arg Arg Lys Ser Leu Trp Phe Arg	
65 70 75	
CTA AGG AAG ATA CTT CTC TGT GTT TTG GGG TTC TAC ATT GCC ATT CCA	290
Leu Arg Lys Ile Leu Leu Cys Val Leu Gly Phe Tyr Ile Ala Ile Pro	
80 85 90	
TTT CTT GTC AAA CTG TGT CCT GGG ATA CAG GCC AAA CTG ATA TTC TTA	338
Phe Leu Val Lys Leu Cys Pro Gly Ile Gln Ala Lys Leu Ile Phe Leu	
95 100 105 110	
AAT TTC GTG AGG GTT CCC TAT TTC ATT GAC TTA AAA AAG CCA CAG GAT	386
Asn Phe Val Arg Val Pro Tyr Phe Ile Asp Leu Lys Lys Pro Gln Asp	
115 120 125	
CAA GGT TTG AAT CAC ACC TGC AAT TAC TAC CTC CAG CCC GAG GAT GAT	434
Gln Gly Leu Asn His Thr Cys Asn Tyr Tyr Leu Gln Pro Glu Asp Asp	
130 135 140	
GTC ACT ATT GGA GTC TGG CAC ACC ATT CCC TCT GTC TGG TGG AAG AAT	482
Val Thr Ile Gly Val Trp His Thr Ile Pro Ser Val Trp Trp Lys Asn	
145 150 155	
GCC CAA GGG AAG GAC CAG ATG TGG TAT GAG GAT GCT CTG GCT TCT AAC	530
Ala Gln Gly Lys Asp Gln Met Trp Tyr Glu Asp Ala Leu Ala Ser Asn	
160 165 170	
CAC CCC ATC ATC CTG TAC CTG CAT GGG AAT GCA GGC ACC AGA GGA GGT	578
His Pro Ile Ile Leu Tyr Leu His Gly Asn Ala Gly Thr Arg Gly Gly	
175 180 185 190	
GAC CAC CGT GTG GAG CTG TAC AAG GTG CTG AGT TCC CTT GGT TAC CAC	626
Asp His Arg Val Glu Leu Tyr Lys Val Leu Ser Ser Leu Gly Tyr His	
195 200 205	
GTG GTC ACC TTC GAC TAC AGA GGT TGG GGT GAC TCA GTC GGA ACA CCA	674
Val Val Thr Phe Asp Tyr Arg Gly Trp Gly Asp Ser Val Gly Thr Pro	
210 215 220	
TCA GAG CGA GGC ATG ACA TAT GAT GCA CTC CAT GTT TTT GAC TGG ATC	722
Ser Glu Arg Gly Met Thr Tyr Asp Ala Leu His Val Phe Asp Trp Ile	
225 230 235	
AAA GCA AGA AGT GGT GAT AAT CCT GTG TAT ATC TGG GGC CAT TCG CTG	770
Lys Ala Arg Ser Gly Asp Asn Pro Val Tyr Ile Trp Gly His Ser Leu	
240 245 250	
GGC ACT GGA GTG GCA ACA AAT CTG GTC CGG CGC CTT TGT GAG CGA GAG	818
Gly Thr Gly Val Ala Thr Asn Leu Val Arg Arg Leu Cys Glu Arg Glu	
255 260 265 270	
ACG CCA CCA GAT GCC CTT ATA TTG GAG TCT CCG TTC ACA AAT ATT CGT	866
Thr Pro Pro Asp Ala Leu Ile Leu Glu Ser Pro Phe Thr Asn Ile Arg	

275	280	285	
GAA GAA GCA AAG AGT CAT CCA TTT TCA GTG ATA TAC AGA TAC TTC CCA Glu Glu Ala Lys Ser His Pro Phe Ser Val Ile Tyr Arg Tyr Phe Pro 290 295 300			914
GGC TTT GAC TGG TTC TTC CTC GAC CCC ATT ACA AGC AGT GGA ATT AAA Gly Phe Asp Trp Phe Leu Asp Pro Ile Thr Ser Ser Gly Ile Lys 305 310 315			962
TTT GCA AAT GAC GAA AAC ATG AAG CAC ATC TCC TGT CCC CTG CTC ATC Phe Ala Asn Asp Glu Asn Met Lys His Ile Ser Cys Pro Leu Leu Ile 320 325 330			1010
TTG CAC GCT GAG GAT GAC CCA GTT GTA CCC TTT CAT CTC GGC AGG AAG Leu His Ala Glu Asp Asp Pro Val Val Pro Phe His Leu Gly Arg Lys 335 340 345 350			1058
CTA TAC AAT ATT GCT GCG CCA TCC CGA AGT TTC CGA GAC TTC AAA GTC Leu Tyr Asn Ile Ala Ala Pro Ser Arg Ser Phe Arg Asp Phe Lys Val 355 360 365			1106
CAG TTC ATC CCC TTT CAC TCA GAC CTT GGC TAC AGA CAT AAG TAC ATC Gln Phe Ile Pro Phe His Ser Asp Leu Gly Tyr Arg His Lys Tyr Ile 370 375 380			1154
TAC AAG AGC CCA GAG CTT CCA CGG ATA CTG AGG GAA TTC CTA GGG AAG Tyr Lys Ser Pro Glu Leu Pro Arg Ile Leu Arg Glu Phe Leu Gly Lys 385 390 395			1202
TCG GAA CCA GAG CGC CAG CAC TGAGCCTGGC CCGTGAAGGA GCATGGAGAC Ser Glu Pro Glu Arg Gln His 400 405			1253
CCACCTTCCT TCCCTCTCC CTGAACAGCA GTCTGGCACC CAGAACGCTCA GAGTGCCACC			1313
ACCTGTGGTG CTCAGGAGCC CAGCCTAGAA AGAGGACTCC GACACAGCGG GCAGAGGCTC			1373
CACAGACGGA TCTATGAGGA AAATACGGTG GCAGGCAGGC AGGCAGGCGA CCCCCCTGACC			1433
CTCTGGTGGC CGCTGTATCT GAGCCCTTTT GGGAAAGGCTT ATAGACAACA GGTGGAGCCC			1493
ATACGCTGGG CATAGGGAGC CTGGGAAGGG CTCAGGAGCT CAGGACCACT CCAGGCTCTC			1553
TAGCACCAAC GCTTAAATA CAGGAAAAG GTTCTTCTG CCCTTCCTGG CGTACACAGA			1613
ACAGATTCCA AGTGGTCAA TTTGTCCCC ACAGCTCATG TACCTGCTTG CCTTCCTCAG			1673
CTGTCCCTGC CTCTCCTGGC ATCTGTACAC CCACAGTGAG GGGCACCTGG ACTTGCACCTT			1733
CCATTCTGCC CACCTGTCTG TCACCTAAC TGGCCGTAGA CTGAGCATTT ATTTAAGAAT			1793
AAAATCTCGG TGGTGGTCTA TTTGTTTTT TCTACAAAAA AAAAAGTCGA C			1844

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 405 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Ala Gly Arg Gln Gly Arg Gly Met Arg Lys Arg Thr Glu Pro Val Thr
 1 5 10 15
 Leu Glu His Glu Arg Cys Ala Ala Ser Gly Ser Ser Ser Gly Ser
 20 25 30
 Ala Ala Ala Ala Leu Asp Ala Asp Cys Ser Leu Lys Gln Asn Leu Arg
 35 40 45
 Leu Ala Gly Lys Gly Thr Ala Glu Pro His Ser Ala Ser Asp Ala Gly
 50 55 60
 Met Lys Arg Ala Leu Gly Arg Arg Lys Ser Leu Trp Phe Arg Leu Arg
 65 70 75 80
 Lys Ile Leu Leu Cys Val Leu Gly Phe Tyr Ile Ala Ile Pro Phe Leu
 85 90 95
 Val Lys Leu Cys Pro Gly Ile Gln Ala Lys Leu Ile Phe Leu Asn Phe
 100 105 110
 Val Arg Val Pro Tyr Phe Ile Asp Leu Lys Lys Pro Gln Asp Gln Gly
 115 120 125
 Leu Asn His Thr Cys Asn Tyr Tyr Leu Gln Pro Glu Asp Asp Val Thr
 130 135 140
 Ile Gly Val Trp His Thr Ile Pro Ser Val Trp Trp Lys Asn Ala Gln
 145 150 155 160
 Gly Lys Asp Gln Met Trp Tyr Glu Asp Ala Leu Ala Ser Asn His Pro
 165 170 175
 Ile Ile Leu Tyr Leu His Gly Asn Ala Gly Thr Arg Gly Asp His
 180 185 190
 Arg Val Glu Leu Tyr Lys Val Leu Ser Ser Leu Gly Tyr His Val Val
 195 200 205
 Thr Phe Asp Tyr Arg Gly Trp Gly Asp Ser Val Gly Thr Pro Ser Glu
 210 215 220
 Arg Gly Met Thr Tyr Asp Ala Leu His Val Phe Asp Trp Ile Lys Ala
 225 230 235 240
 Arg Ser Gly Asp Asn Pro Val Tyr Ile Trp Gly His Ser Leu Gly Thr
 245 250 255
 Gly Val Ala Thr Asn Leu Val Arg Arg Leu Cys Glu Arg Glu Thr Pro
 260 265 270
 Pro Asp Ala Leu Ile Leu Glu Ser Pro Phe Thr Asn Ile Arg Glu Glu
 275 280 285
 Ala Lys Ser His Pro Phe Ser Val Ile Tyr Arg Tyr Phe Pro Gly Phe
 290 295 300
 Asp Trp Phe Phe Leu Asp Pro Ile Thr Ser Ser Gly Ile Lys Phe Ala
 305 310 315 320

Asn Asp Glu Asn Met Lys His Ile Ser Cys Pro Leu Leu Ile Leu His
325 330 335

Ala Glu Asp Asp Pro Val Val Pro Phe His Leu Gly Arg Lys Leu Tyr
340 345 350

Asn Ile Ala Ala Pro Ser Arg Ser Phe Arg Asp Phe Lys Val Gln Phe
355 360 365

Ile Pro Phe His Ser Asp Leu Gly Tyr Arg His Lys Tyr Ile Tyr Lys
370 375 380

Ser Pro Glu Leu Pro Arg Ile Leu Arg Glu Phe Leu Gly Lys Ser Glu
385 390 395 400

Pro Glu Arg Gln His
405

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 855 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (vii) IMMEDIATE SOURCE:
(B) CLONE: HW074

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 7..300

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: complement (64..365)
(D) OTHER INFORMATION: /label= SAC_24464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GTCGAC AGC CCT CGA GGG AGC AGA CGC CGC GGG CCA CTG GCT TCC TCT 48
 Ser Pro Arg Gly Ser Arg Arg Arg Gly Pro Leu Ala Ser Ser
 1 5 10

ACT CAG GAA CCA CGG ATG TCA CCG CCC AGT CAG CTG TGT CTC CTC ACC 96
 Thr Gln Glu Pro Arg Met Ser Pro Pro Ser Gln Leu Cys Leu Leu Thr
 15 20 25 30

ATT GTC GCC CTG ATT CTG CCT AGT GAA GGG CAG ACA CCA GAA AAA CCC 144
 Ile Val Ala Leu Ile Leu Pro Ser Glu Gly Gln Thr Pro Glu Lys Pro
 35 40 45

AGA TCC AGT TTT ACA GCG CAC CAG AGT TCT GTG ACT ACT CAT GTC CCA 192
 Arg Ser Ser Phe Thr Ala His Gln Ser Ser Val Thr Thr His Val Pro
 50 55 60

GTT CCA GAT CAA ACT AGC CCA GGA GTC CAG ACC ACT CCT CCC ATC TGG 2400

Val Pro Asp Gln Thr Ser Pro Gly Val Gln Thr Thr Pro Pro Ile Trp		
65	70	75
ACC AGT GAA GCT GCG AAG CCA CAG GAA GCC AGA CAG CAG CCA AAA CCA		288
Thr Ser Glu Ala Ala Lys Pro Gln Glu Ala Arg Gln Gln Pro Lys Pro		
80	85	90
AGA CCC AGC AAC TGACCGAAAT GGCCACTGCG AATCCAGTGA CAGATCCAGG		340
Arg Pro Ser Asn		
95		
GCCACTTACA AGCAGCGAGA AAGGTACCCC GGCACTCTCC AGGATCAAAT CTCCCAGCCC		400
ACCCAAAGGT TACATGCCTC CATCCTACAT TGAGAACCCA CTGGATCCCA ATGAGAACAG		460
CCCCTTCTAC TACGACAATA CCACCCCTCCG GAAACGGGGG CTGCTGGTGG CGGCAGTGCT		520
GTTCATTACT GGAATTATCA TCCTCACTAG TGGGAAGTGT AGACAGTTCT CTCAGTTATG		580
CCTGAATCGC CACAGGTGAG TGGGAGCCAG CACCTGATG GGCACCCCAA CTGGAGCCGC		640
CATACCATAC CAGTTCACCA CCCCTGCCTC CCTCCCTCTG CTCCAAGAGC CAACAGAGTG		700
GTCAACATAA ATGGATCCTC AAAGGAAGAG GCCACCCGGAG GGAGCCAGGC CTAAGGCTAA		760
ATGGTCTTCC CACCTTGAGG AGAGAGGTCT CCCCAGGCAC TGCTGTGATC CTGCCTATCC		820
TGTTCAGATA AATCCACATG GTCTCTCTTC AAAAAA		855

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Ser Pro Arg Gly Ser Arg Arg Arg Gly Pro Leu Ala Ser Ser Thr Gln			
1	5	10	15

Glu Pro Arg Met Ser Pro Pro Ser Gln Leu Cys Leu Leu Thr Ile Val			
20	25	30	

Ala Leu Ile Leu Pro Ser Glu Gly Gln Thr Pro Glu Lys Pro Arg Ser			
35	40	45	

Ser Phe Thr Ala His Gln Ser Ser Val Thr Thr His Val Pro Val Pro			
50	55	60	

Asp Gln Thr Ser Pro Gly Val Gln Thr Pro Pro Ile Trp Thr Ser			
65	70	75	80

Glu Ala Ala Lys Pro Gln Glu Ala Arg Gln Gln Pro Lys Pro Arg Pro			
85	90	95	

Ser Asn

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HW075

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION: complement (3785..4014)
 (D) OTHER INFORMATION: /label= SAC_24466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GTGCGACATGG CGAAGTACTC TAGCCTGGAA GCCAAGCTCT	60
GCCAGGTTGA AAGTAAATAC TTGATACTGC TCCAAGAAAT	120
GAAGACACCA GTTTGCTCAG AAGAACAGGG CCCTGCCAGG	180
GATGTCATAG CCCAGTTGTT GGAGGACGCT CTGCAGGTTG	240
AGAGCCAAGA GCAGCCAGAG CAAGCCTTG TCAAGCCTCA	300
TCTGGTCAGT GAGTCGATA TCTACGGGTT TAGGACTGTC	360
CCTGACGATG ATGAGGAAGA GAAATTGGTC GCCAAGGTCC	420
GAGCATTGGA CCTGAAGACT CTGTACCTCA CAGAAAACCA	480
GGAAAGTTCC ACTGGGGTCA AGTGGGAAAA CTATTTGCA	540
AGCACAATGA ACAGGGAGAT GGTGTGCTCT CCTGAGCTGA	600
AAAACCTGAT CCGAGCAGGC ATTCCCCATG AGCACCGCTC	660
CAAGGTGTGG AAGTGGTGTG TTGACCGTCA CACCAGGAAG	720
TTCAAGGACA GCATGGAGCC AGGCTACTTC CAGGCCCTAC	780
TCCAGAAGGC TCTAGAGAAA CAGAACCCGG CCTCCAAGCA	840
GATTGAGCTG GACCTGCTTC GGACTCTGCC CAATAACAAA	900
CATTACTCCA GCCCCACGTC AGAGGGCATA CAGAAGCTTC	960
GCAATGTCCT GCTTGCCTTC TCATGGAGGA ATCCGGATAT	1020
TGGCTACTGC CAAGGCCTAA ACAGGTTGGT GGCAGTGGCG	1080
CTCCTTTACC TGGAACAAGA GGATGCTTTC TGGTGTCTCG	1140
TTACCATTTGT GGAAGTCTTC ATGCTCGAG ACTATTACAC	1200
AAAGACTCTA TTAGGATCCC AGGTGGACCA GCGGGTGTTC	
AGAGACCTCC TGAGTGAGAA GCTGCCTCGA CTGCACACCC	
ATTTGAGCA GTACAAAGTG GACTACACCC TCATCACCTT	
CAAATGGTTT CTGGTGGTAT TCGTGGACAG CGTTGTCAGC	
GACATCCTCT TTAAGATATG GGACTCTTTC CTTTATGAGG	
GACCAAAGGT TATTTCCGT TTTGCCCTGG CACTTTTAA	
ATACAAGGAA GAGGAGATCC TGAAGCTGCA GGATTGATG	
TCCATTTCA AGTATCTCCG ATACTTCACT CGCACTATCC	
TTGATGCCAG GAAGCTGACC AGCCTCCTT TTGGGGATCT	
GAACCCCTTC CCCCTGCGCC AGATCCGGAA CGGGAGAGCC	

TACCACTTGG AGAAGGTCCG GCTGGAGCTG ACAGAGCTGG AGGCCATTG AGAGGACTTC	1260
CTGCGTGAGC GGGACACTAG CCCTGACAAA GGCGAGCTGG TTAGCGATGA GGAGGAAGAC	1320
ACTTGAAATGA ATCCCCACCC CAGGATGCTG CCTTCCTTCT TGCCCTCCCT CATAACCAA	1380
AGTAGCAAAG GCGCATCTGC ACATCAGCTG TCAGAGTGAA ACATCTACAG CCTCTGGCA	1440
CCTGCGGGC AGATGTCCAA AGCTAAGCTG CACTTTCTCG TCTGCCATGA GGGCAGGGT	1500
CTGATGGCTT TACAGCCATT TCCATGCCGT GGCATTCACT CATATGCGTC ATATGCTTGC	1560
TGCCTGATGG GTGAGTCACC AGGCGACTGT TTCCAAGGGC CTGTTACAT CATCTGCCAG	1620
TTGTATGTTT CACCTACAGA AACTGTTGA CATTTCCTG TGCGTTTCT TTTTATCCAA	1680
GGGCAACTCT GTGGAGGAGT GCACATGGAG CTGCAGCGTG GCTGCATCCA GGGGTAAAAG	1740
GTCACCATAA GAAGAGGGAC CTCTTTAAAA AAAAGCGAGC ACAGAACTGG CCTCCCTAGA	1800
GAGCGTGGGA GCCCTCTGCT GGTGGCTCG CACTGCCAGC CACTATCCCT TCTGGACTAA	1860
CCTTTGCCCT CCTATACAGC CTTTCAGAT TGTAGCACTC ACGCTGCTCT GCAGCCAGCC	1920
CCACACTTCT CATTGCCAGC TATTCTGCCA GATGCTGTC CCAGCTTACA GTGGGGCTAG	1980
CGCATCTGGG AGGTGACTTA TAGACAACAT TCTCCAAGTG TGGCTAGATT GGCAGTCCAA	2040
AGGAACCTTA CAGTAACCCA CCCCTGCATA AAGGAACACAA GGAAACTCCT ATCTGTGGCT	2100
TGTGGGCTCC TGGATGGCAG TGGCCAGGGC TCTAGAATCT CTTCTGCCCA ACAGCTGGT	2160
GGGGAGTAGA GCTGACTGCC AGCTTCTAC ATCTGGAAGC ACCTTTGCTT GGGAAACAAGA	2220
GTAATGAGTT CTCCTAGTCT CTGTGTTGCC TGGATCATCC TTGTCCTTAA CAGGGATCTG	2280
AGGACACTGT GGCCCTCTGGT ATAGCAGACT CTGGGGACTT GGAACACTTC CTTCTGAAG	2340
CCCAGAGAGG GTCTGAACAA AAAAGGTTAT TTTTGCTCAG TCCCAGAGCA TCCCTAATGG	2400
TGGCTGTTAT GAGAAAACAT CTTCTTACAC AGTATTATGG AACACACAAG GAAACAGCCT	2460
CAAGTGGACT ACTTTACACT ACCTAGGGAA AAGAAATTAG AAACAATCCT TAGTGTAAAC	2520
ACACTCAGAC TGAGGAGTGG AGCAAGACAG TTTCGAGAAA CGCTTTTCC ATGACCCGTT	2580
TTCCCTGTTT TGCTGTCCTGC TTCTCTAGCAC TTGAATGGCT GAGTCCATTTC TCAGCATCTA	2640
AATTGCTTC ACTTCTCTAA AGTTGCTTCA TATATTACCA TGAAAAGGA GCTGGCTCT	2700
ATATTTAGCC AATAGCCCGT CTCTTTTCAG GTATCAGAAA TGTCATCCTT GTGTCTTGA	2760
GATGATGGTT TGAGGCCCGG CTTCTTGAAG AAGCTGTCTG GAGCTGGACA GTGATCTATC	2820
TCACCACTGT TCCTAGGCCT CCCTGAGACC AAATGCTGGA AGATGCCCA CCCCCTGTAA	2880
GATGCCGGCT GTCAGCCTTG GGGACAGCTG TTAGGAGGTT AGAGTTGGAG CCCCATGGCT	2940
TAGCTCCAGC CGCTCTGATT TCGGTTGTCA TGTCATTTC CTACCAGAAG ATCCAGTCCA	3000
AATAAGTATT TGGTGTGGAT GCTCTCAGTG GAGCATTGG TGTGGATGCT CTCAGTGGTG	3060
GGTTGCTTTC GCCCTGGCAC CAGTGGAGGC ATCTTTAAGT ACTTGGTGAT GCTGAGGACA	3120

GGACCATGTT CCTGGCATGC GGGGCCCTGG GTTCCATCCC AGTGATGAAA	AAAAATCTTC	3180
AGTATGTGGG GATTGTGGGG AGGCGCTGTT CTGCCATCCC CTGAGAGACA	GCATTAGTTT	3240
CTCAGGCAGT TAGTATCAGT GCCCAGGTAA AAGTCTCAAG AGGTCCCAA	GGGACTCTCC	3300
TCCCTGGAAT AAATGACTCG ATGTCTGCAG AGCGGAGAAG GGACGGTTGC	CCTCTTTCCA	3360
GTTTGGGGAC AGAATAACAG AGATTCATCC CAGAGGCACA GCCCCAGTGG	TTGAGGCCATC	3420
GTCTCTCATG CCCTCGTCAC TGAGATTGTC TTTACCCCTCC AGTACTCCTG	AGACTCCAGA	3480
CTTCTACCAG ACACCATGGC AGGTACCCCT AAGGTCAGTG GCTGCCTCAG	GCTGCTTTTC	3540
ATCTAAACCT TTACCCAGCA TGCAACCCAT GGCTCCTGCC TGGTGAGCCT	TGTGGGCTGA	3600
GAAACCCAAA GCACAGCCTC CAGCGCGTGG GTCCAAATGC GTGTGCCACA	GTAGGGGAGC	3660
ACCCCTGCCCT CAGCACCCCA TATGGTGGGA CTTGCCAGTA TTCAACTGT	TGATACTTTT	3720
ATATTTTCAC TACATTTTAT ATTTTTATAG ACTATTTTAT ATTAAGGTTT	TTTCTAGATT	3780
CTGTACAAC TTTATATAAC AAGTTCTATT TTGTGTGCAC ATCTCCCTG	TATGTATTTA	3840
TAGCAACCCA AGCCTCTCAA ATTCCAGGTC CCTCTTGTGC CACCTTTCC	CCTTAGCCTT	3900
GACTGTCACT CTCTTCTGCT CACCGAGGTA GCCTCGGGGG CTACTTCTAG	CCACCATGAC	3960
AGCCAGACAG CAGGAACTGG TGTTTGTCACT GTGTGGTCTG TTGATACAGG	AAGTACTCTG	4020
GGCAGTAACC CAGTAGCTAT GTTACTGCAC AAGCCCTCT CGCTTAGTGC	AGTGATGTCC	4080
TGGTGCAGCC ACCTGTGGGC GGGTGGCTGG ACCCATCACG AAAGTCCTTG	AAGACAGAGG	4140
CTAGATGAAA GCCCAGTGTC TGAGGTCTT CTGTGGCAA CTGGAGGACT	TGAGGGCACA	4200
CTGCCAAGTG ACTGTCTTT TATATCCTAG CAGCTCTGT GCTCACCCCTT	GAGTTAAATG	4260
TTAGACTTTT AAAGGAAGAA ATAAACTAAT TTGTATTACA TTCTGCCTCG	AAAAA	4315

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1668 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HW076

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: complement (42..281)
 (D) OTHER INFORMATION: /label= SAC_24409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GTCGACTTTT GCCTTTAAA TTCTGTTAC TTAGCATATG TACACGTAAA AGAGAAATCA	60
CCCTTAGATC CCACCCAGCA GAAAACATGC ACAAAACCAA GGTATATGTG AAAGGGAGGG	120
CCCCAGCCCC AAGTTAGCAG TTGGGATGGT GCAATCCTGT GAGTCACAAG CCCATGGCAA	180
GAGGGCTGGA CTAAAGTTTC AACACAGCCA GAACCCCTGC TGCTGGCCCT AAAATAAGCG	240
TGCACCATAG CCAAAGGTCT GTTTGATGCC CTCAAAGTAG TACCGCTGCC AGCCTTGCG	300
TGTCCGCTCT TCCTCGGGAG CAGGGATGCC GCGGCCCTCC ATGCACAGCT CTGTCTCTCC	360
ATTCTTATCA ATGAAGGTCA AGGTGATGGT CGCGAAGTGC CCCTCTGGCC ATGACTTAAA	420
CCTCCACTTC ATAGCAATAT GTTTCTCAGG AACCAAGTCA GTAAACTCCC CAGTGACGTT	480
ACCATCGACC ATGTGAAACT TCCCCTCTCT GTCTGCTTCC AAGGCCGAG GAGCATGGGT	540
AAAGGCTGG ACCAGCTCCT GCGTGGTGAA CACTCTGTAG AGCTCCTCTG GAGAGGTCAG	600
GAAGGTTTCT TTGAGGGTGA TCTTACAAGT GGGTATTTTG ACACCAACAG GTTTGGCCTG	660
GCTTTTGAA GGAGCACACT TAGCCTTGCA CACTTCCGTT TTTAGTGCTG GTTGGCCAC	720
TGGGTCTACT GATTCTCCAT TCACTGTGGG CAAGATCATG CCCTGAGTAA ACTCTGTCTT	780
GAGGGTGCTG ATGTAATTC CCACTGCTTC TCTGAGAAGT TTCACCCCGT CTTCCCTCAT	840
TAAGGCCACG AGACTTGTGT CAGGCTCATC TTTGGCAAGG CTGCTTCTTA GAGCCCTTGT	900
TATGGCAGCG CTCCATCTAG GAAACAGCAG TCAGTCTCTC CTGCTCACTG TTCTCCCTCT	960
CTGTCCTCAA GTCTGTCAGT GCTCGTGGC CTCTGGCTCT TCCCTTGAGG GAGGGAGCGG	1020
CTGTTCTGCC TGCTTCACCG AGTCTTCACA AGCTGAGGGG ATGAGGCCAG GTTAGTACCA	1080
GGGACCAGCA ACCTTCAGG GCTCCTTGGG GGTCTCAGGT CCACACACAG TGAGCATCCC	1140
TTGCCAGGTG CCCCATGTAT CTGTCAGTGC TGAGACGCCA AACACACAAC CTGTTCCCAG	1200
CTGCTGCTGG GGGCCACTGT GACCGAGGAG AGTGTGGGGT TGCCAGGGAG AGCGCTGTCC	1260
CTCTGACAGC CTGACCAAGAT GATGTAGCTT TGAAAGCCGG CAGCATGTGA GTAGCAAGAT	1320
GTGACCTTGA GCTAGCTGAG CAGAACACAG GTGGATGGGC AGAGGCCCCC ATCCTGGCGA	1380
GCTGAGCCTG GCTGTGTCT GTCAGGACGC CCTACTCTGT GACCCCTACCC TGTGATCTGT	1440
GAAGTGGTGC AGTCGGAAGA CGAGGCTGGA GTCCCTTACA AGTTTCTACA CTAGATTGTA	1500
GCCAGGTTTT CTCCCAGGCC TTAGGCTTTG GTTTACTTTT AATTTAATT TCACTGTTAC	1560
CCTTGACTAT TGTCCCTTTT GTTGCAGTGT TGGAGAGGCA GGAGGTATTT GTGCCCTCATC	1620
TATTAATGCA AAAAAATTAA ATAAATGTA CAATAAACGT CCTAAAAA	1668

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1019 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HW078

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION: complement (211..743)
 (D) OTHER INFORMATION: /label= SAC_24345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GTCGACGCCA GCGTGAGCGC CCTGCAGCGC CTGGTGGAGC AGCTGAAGCT GGAGGCCGGC	60
GTTGGAGAGGA TCAAGGTCTC TCAGGCAGCT GCAGAGCTTC AGCAGTACTG CATACTAGAAT	120
GCATGCAAGG ACGCCCTGCT GCTTGGTGTT CCGGCTGGAA GCAACCCCTT CCGGGAGCCC	180
AGGTCCCTGTG CTTTACTTTG AAGACTGGGA AGAACGCTCTC TGAGGAACCT GTGTGTGCAT	240
GGTGATGGAT GACTACCGCC AAGTCCAAG AAAACAGATT TCAAGAGCCA AATCATTTC	300
TCTGTGGCCT GGTCTTAGGT CAAAATTCTA CAGAAATCAA TGTTTTGTCT TATTTTTAA	360
CCTCATTACC AAACTCACTG GGTGCATCTC TCAGTCAAGC CTGTGCGGCC CTGCCCTGGGA	420
TGGAGGCATG TTTTGTTTAC TGGGTATTTG CATTCTGGA TGGAAATGTT GTATTTCCGA	480
AAACCTGAGTA TTTGTAATTTC TCCTAACATT TTATATACTGT AATAAAAAAT TTTCATAAAA	540
ATTTACAGTT ACTAAATTAG ACAAAAGTATA AATTGGGAA TGATTGATAT GCTGGTTTCG	600
TAAAGGAGGC CTTTCCAGTC CCAGTGAGCA AACGGTCTGA CCTGGACGGG AAGCTGGGA	660
GCCGCTCCTT AGCACACGGG GCATGGATGT GTTGTAGGT GGCCCTCCCG TGTGAAGCCA	720
TTAGAACTTT CTTTAGTTCC TGTACTCTAC AACTTATAAT TGTGTCTGAT GCTTTGAAAA	780
GTGTGCTCAT GCCTTAAAAA ATGTTAAAT GTGATCTACA CTTAGAACGT TGCAATTGGT	840
TAAAAACAAA ATATGAAGAT ATTATAACCT AAAAGAATTC ATGTCACACA TATTTTATTG	900
GGGGTGATGT GCCTTGATT TAATTGGGA CACTTTAGA AGGAAAGTTT GTGTTTGTGA	960
TTATCTTGGA AGAGCTTGGA AATAAAATT TTGCCTAATT CATCATTTC CATGAAAAA	1019

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 961 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HW080

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 629..919
- (D) OTHER INFORMATION: /label= SAC_24033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GTCGACGCTG	GGCAAAAGAA	GGTTCCACCA	GAGCCTGTGG	GTTTGTCCCTT	AGGCTAGAGG	60
CCCCAAGATT	TGGAACCTGG	TGGAATCAGT	AGGAGGGACA	TTGAAGCTCA	CAGATATATC	120
ACACGTTGGT	CAGTTGCTTC	TGCAACTGGT	CCGTTAGGTG	CTGTGGGACG	AGCCCTTCC	180
TACCTCTTC	AGCTTCTACA	TCCACTGTCT	GCCTGTGTCT	CAGTTTACAT	CTTCCTTTG	240
AATATGGAAT	CTCAAATAGC	CCAGGCTAGC	TTCAAATTG	TTAAGTAGTT	GAGGACAACC	300
TCAATCTTC	TATTCGCTGC	CTCCACCTCT	CTCAGTTTAC	CTTTTTTTTT	TTTCTCCCTA	360
GGATTAAGTC	CGGTACAGGC	CCAGAGTGGT	AAGCCATAAC	ACCCCTGGTC	TTTCTCTCTT	420
CCTCTCAAGA	TTTCCTCAGG	CTACCCCTTT	TCCTCTAGC	TCTCTCTCTC	TGCTAACGCC	480
GAGCCCTGAT	TGTTAACCTG	TGTCTCCCTC	TTCATCCTTC	TGAGACAATT	ACCCAGGATG	540
CGAATGTTCC	TCTGTGAGCC	CGGGTGTACT	GGCTGGGATT	GTGCTGGGCG	ACTTGGTGCT	600
GAECTCTGCTC	ATCGCCCTGG	CGGTGTACTC	TCTGGGCCGC	CTGGTCTCTC	GAGGCCGAGG	660
GAECTGCAGAC	GGGACCCGGA	AACAGCACAT	GGCTGAGACT	GAGTCACCTT	ATCAGGAGCT	720
TCAGGGTCAG	AGGCCAGAAG	TATACAGTGA	CCTCAACACA	CAGAGGCAGT	ATTACAGATG	780
AACCCACCC	ATGCCACCA	ACAACCTGAT	GCCCCGATCC	ACTCATTCCA	GACGCTTACT	840
CAACAAACCC	TCCCTGGGAT	CAGGACTCCC	GCTGGAATAA	ATATCCACAG	AGTGCCCTCT	900
GGGAGATATC	TGACCTTGTG	CCGTTTCTGT	CCCCAAATAA	AAGACGAAGC	AAAAACAAAAA	960
A						961

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1890 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HW082

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 150..569

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1381..1848
 (D) OTHER INFORMATION: /label= SAC_24469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GTG	ACCCGCG	GCCGCGTCGA	CGGACTTGCG	GTTCTTCAG	CATTCTGCC	GCGCACTGAG	60
TGG	CTGTTTC	CTGGAGCTAC	TGTGTTCTT	CGGGAGTGCA	GCAGATCCC	TTCAGAACCT	120
ATTACCAAGA	GCCCCGAGCA	GGACCCACC	ATG CAG TGC	TTC AAA	TTC ATT AAG		173
			Met Gln Cys	Phe Lys	Phe Ile Lys		
			1	5			
GTC	ATG ATG ATC	CTC TTC	AAT CTA CTC	ATC TTT	CTC TGT	GGT GCA GCC	221
Val	Met Met Ile	Leu Phe	Asn Leu	Leu Ile	Phe Leu	Cys Gly Ala Ala	
10	15	20					
CTG	TTG GCT GTG GGA	ATC TGG GTG	TCC GTC GAC	GGG ACA TCT	TTC CTG		269
Leu	Leu Ala Val	Gly Ile	Trp Val	Ser Val	Asp Gly	Thr Ser Phe Leu	
25	30	35	40				
AAG	GCC TTC GGA TCA	CTA TCA TCG	AGT GCC ATG CAG	TTT GTC AAC	GTG		317
Lys	Ala Phe Gly	Ser Leu Ser	Ser Ala	Met Gln Phe	Val Asn	Val	
45	50	55					
GGC	TAC TTC CTC ATC	GCC GCT GGT	GCT GTA CTC	TTT ATT CTT	GGT TTC		365
Gly	Tyr Phe Leu	Ile Ala Ala	Gly Ala Val	Leu Phe Ile	Leu Gly Phe		
60	65	70					
CTG	GGC TGC TAT GGT	GCT CAC TCC	GAG AAC AAG	TGT GTG	CTC ATG ATG		413
Leu	Gly Cys Tyr	Gly Ala His	Ser Glu Asn	Lys Cys	Val Leu Met	Met	
75	80	85					
GTG	TGT TGG ACC CAG	CTC CCC AGG	CCC ACA ACC	AAG GGT	TCC CCC TTC		461
Val	Cys Trp Thr	Gln Leu Pro	Arg Pro Thr	Thr Lys	Gly Ser Pro	Phe	
90	95	100					
ATC	CCT GAC ACC AGC	CTC TGG GAT	CCC AAA ACC	CTA CTC TGG	ATT CTG		509
Ile	Pro Asp Thr	Ser Leu Trp	Asp Pro Lys	Thr Leu	Leu Trp	Ile Leu	
105	110	115	120				
GAA	GCC TCG CTG	TGG GGA	CCC CCT GCC	TCT TAT GGG	AGT GTG CAG	GAA	557
Glu	Ala Ser Leu	Trp Gly	Pro Pro Ala	Ser Tyr	Gly Ser Val	Gln Glu	
125	130	135					
GGT	GTG TAT CCC	TAAAACGTGT	TTCCTTTCTC	CACTCAGTTC	TTTTCCATTTC		609
Gly	Val Tyr Pro						
140							
TCCTCATCAT	CTTCATTGCG	GAGATTGCAG	GGGCCGTGGT	TGCTTTGGTG	TACACCACAA		669
TGGTGAGGCA	CGGGATGGGG	CATGGGAGGA	AAACTGGAGC	AAAGCTCTGA	GAGTTGGTGG		729

TGGCCTGTGA ATGGCTACTT CCCCTACCAAG TCTATTAATA CTGGCCTGAC CCGTCCAGGC	789
TGAACAATTG CTGACATTTC TGGTGGTGCC TGCTATCGAA AAGGACTATG GTTACCAGAC	849
TGAATTCAACC CAAGTGTGGA ACTCTACGAT GGAGGGGGTA AGGTGGGCCG GGAGGAGTTG	909
GGAATGGAGA GGAGAAAAAA ATCAAGGCAC CATCAGTTAC CAACCCCATT TTGTCTGCAG	969
CTGCATTGCT GTGGCTTCAA CAATTACACA GATTTTAACT CCTCACGTTT CGTCAAAGAG	1029
AACAAAGTCT TTCCCTCCGTT CTGTTGCC AACAACACTG ACAGTCATAC AGTTGAACCA	1089
TGCACCGAGG ACAAGGCCAA AAGTATGAAC GTACAGGTAT GTGCTGGTGT GGAATTAGCT	1149
TTTCGTTTG TGATCCGGTT TCTCTGTGTA GCTGTGGATG TCCTGGAACG CGATATGTAG	1209
ACCAGGCTGG GCTTGAACAG AGATCGACCT GCCTCTGCCT CCTGAGTGCT GGGGTTAAAG	1269
GCCACCATCA CCACCCAGCG CCAGTGTAAATG TGCTTAAATG GCTTTACAGT AAGGAGTAAA	1329
GGGGTTGGAG GTAGGGCACT GCCAGCTATA AATACTTTCT TCTCTCTCCC AAGGGTTGTT	1389
TCAAACAGAT TCTGCAGAAA ATCAGAACCA ATGCAGTTAC CGTGGGTGGT GTGGCAGTTG	1449
GAGTTGCCGC CCTAGAGCTG GCTGCCATGG TGGTATCCAT GTATCTATAC TGCAATCTGA	1509
AGTAAGACTG CTTCTTCCTC CTGACTTGTG GTCACATGGA AACCAAGGAAG AGGCACTTGG	1569
CACAGCTAAG CAGCAGCAAT GGGTGGAGAT GAAACGTCAT TTGGGCTGGA GTGGATCTGC	1629
CTTTGCTGCT CTGGACTTCG GGCTAATTAG GGACCACCGC TCGGGCTGTG TCTGTCTTGT	1689
TCTTCCACTA CTGGGGCGAG GGGGCATTG GTCCCAGTCT CTGAGGTAGC CATGTCGCC	1749
CATCTCCTGA GATTCTTGAT GATCCCAGCA CTCCACTGGT GGATGAAGGC ACTTATAGCC	1809
TGGGCATATT CTAGCACTGC AAAGTCATAG AAGGAATGTA CAGAAGGTGT TTTGGAACCTT	1869
ATAAACCAAT GAAAATAAAA A	1890

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Met	Gln	Cys	Phe	Lys	Phe	Ile	Lys	Val	Met	Met	Ile	Leu	Phe	Asn	Leu
1						5			10			15			
Leu	Ile	Phe	Leu	Cys	Gly	Ala	Ala	Leu	Leu	Ala	Val	Gly	Ile	Trp	Val
								20		25		30			
Ser	Val	Asp	Gly	Thr	Ser	Phe	Leu	Lys	Ala	Phe	Gly	Ser	Leu	Ser	Ser
								35		40		45			
Ser	Ala	Met	Gln	Phe	Val	Asn	Val	Gly	Tyr	Phe	Leu	Ile	Ala	Ala	Gly
								50		55		60			

Ala Val Leu Phe Ile Leu Gly Phe Leu Gly Cys Tyr Gly Ala His Ser
 65 70 75 80

Glu Asn Lys Cys Val Leu Met Met Val Cys Trp Thr Gln Leu Pro Arg
 85 90 95

Pro Thr Thr Lys Gly Ser Pro Phe Ile Pro Asp Thr Ser Leu Trp Asp
 100 105 110

Pro Lys Thr Leu Leu Trp Ile Leu Glu Ala Ser Leu Trp Gly Pro Pro
 115 120 125

Ala Ser Tyr Gly Ser Val Gln Glu Gly Val Tyr Pro
 130 135 140

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HW083

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: complement (1950..2181)
- (D) OTHER INFORMATION: /label= SAC_24528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GTGACCCAC AATGCCCGA GCACCTGGAA TCACAGCAGA AACGACCAA TCCTGAGCTC	60
CGTAGAAATG TGACCATCAA AACTGAACTC CCACTAGGCG CACGGCGAAA GATGAAGCCA	120
CTGCTCCAC GGGTTAGCTC ATACCTGGTG CCCATCCAGT TCCCGGTGAA CCAGTCCCTG	180
GTGTTACAGC CCTCGGTGAA GGTTCCCTTG CCTCTGGCAG CATCTTTAT GAGCTCAGAG	240
CTTGGCCCGTC ATAGCAAGCG AGTCCGCATT GCACCCAAGG TGCTGCTATC CAACGAAGGG	300
ATAGCCCCAC TTCCGCCAC AGAACCCATG AAGGAGGAGA AACCCCTGCT TGGAGAAGGG	360
CTATTGCCTT TGCTTCCTAT TCAGTCCATT AAGGAAGAAG TAATTCAAGCC TGGGGAGGAC	420
ATACCACACT TAGAGAGGCC TATCAAAGTG GAGAGCCCTC CCTTGGAAAGA GTGGCCCTCT	480
CCGTGTGCAT CAGTGAAAGA GGAACGTGCC AACTCCTGGG AAGATTCTTC CTGCTCTCCT	540
ACCCCAAAGC CCAAGAAGTC CTATTGTGGG CTTAAGTCCC CAACACGGTG TGTCTCAGAA	600
ATGCTGGTGA CAAAGCGGAG AGAGAAGAGA GAGGTGAGCC GATCTCGGAG GAAGCAGCAC	660

CTTCAGCCAC CCTGTCTAGA TGAGCCTGAA CTCTCTTCT CAGAGGACTC CAGCACATT	720
CGGCCAGCCA TGGAGATCCT GGCAGAGTCT TCAGAGCCTG CACCACAGCT CAGCTGCCCT	780
CAGGAGGAGG GAGGGCCCTT CAAGACCCCC ATCAAGGAGA CATTGCCTGT CTCCTCCACT	840
CCTAGCAAGT CTGTGCTCTC TAGAGACCT GAGTCCTGGA GGCTCACACC CCCAGCCAAA	900
GTTGGGGGT TAGATTTCAAG CCCAGTACGA ACCCCCCAGG GTGCCTTG CGCTCTGCCT	960
GAATCGCTGG GGCTTATGGA GCTGAATACC ACACCTCTGA AAAGTGTTC CCTCTTCGAC	1020
TCACCCCCGGG AGCTCCTTAA CTCAGAAGCC TTTGACCTTG CCTCTGATCC CTTTAGCAGT	1080
TCTCCACCAC CACATTTGGA AGCCAAGCCA GGCTCCCCCG AGCTGCAGGT CCCCAGCCTT	1140
TCAGCCAACC GTTCTCTCAC AGAAGGCCTT GTCCCTGGACA CAATGAATGA TAGCCTCAGC	1200
AAGATCCTTC TAGACATCAAG TTTCCCTGGC CTGGAGGAGG ACCCTCTGGG CCCTGACAAC	1260
ATCAACTGGT CTCAGTTCAT CCCTGAGCTG CGATAGAGGC AGGGTCTTAC CCTTGCCACT	1320
CAAGCCACCA GTTATCCTGG CACTTGTGTG GCTGGATAGT GCAAGGCTCA GTGTACCCCA	1380
AACCGTCTGA GGGAGCTAGC AGGCAAGGGC TGAGCGGTGC CCTTTGACCT AATTATGCCA	1440
AGGTAAAAGC CACGTCTAAG CCACTGCTGG GACCTATGCA AGCAATAGGA TCTCCCAGAG	1500
TCCTCCACTC CCTGCTGGCA AGTGAAGTGG GTGTGACAGA GCCGTGAGGA CCAGGAAATG	1560
CCCACCCATT AGTCACCTGC TGCTCCTGGC AGGATAACCC TTGTAAATGG TGTCAGTTCC	1620
CCAAGTTGTC CTGTAATTAT AAATGTAGCC ATATTCCCTT AGCTCTCATT ATCCAGAGAC	1680
TGCCAGGATG GGTAGGGTGA CAAGGGTTG CATTAGCTTC TGCTTGTGGC CTTTGGGGC	1740
AGGACTGCA GTTCAGCCTC TTCACACTGT GGGTTCTGCT GTAGGCTTCT AGACACACAG	1800
GTGTCTTGC CAGGACCCCA CTTACTGCCCTTCCCTCACA GCTCCCCCTG GTTCTAAGCC	1860
AGTGGTACTG CATGAAGAAA TCCTGCGCA AAGCCTATTG GCTCTGGGTG TGTGGGGACG	1920
GGTGTGCCCTG AAGCAAAGC ATGGGTACTC ACGTGAGTCC TTTAGGTGTT TCTCTGATCG	1980
TGTTCCAAT CATGCCAGGG AGTCTAGCAT TGAGAACTCA GGCTGAGGCC TGAGGAGGAG	2040
GAGGAAGTGA CCACTGACTT GCCTGGCTTC CTTAGCTTGC ACCTGAGTTT TGCAAAAAGC	2100
CACCCCTAGAC CCCACTCTAC AAGCTAGCAC AAGAACACTA CTGTAACTAC CTACTGAATA	2160
AAGCCCAGGT GGCTGAAAA A	2181

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: HW084(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: complement (163..391)
(D) OTHER INFORMATION: /label= SAC_24854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TTTTTCCACC AAGAGGGAGT CCTTTAACAG ATTGCACAGA CAGACACAAC AGGCCAGCAC	60
CCTGCTTGCA GGCCCAGGCG CTTTGCCAGC AGATGCAATG GCCTCCCCCA CCTGGGTGTG	120
GGCCGCAGGG TGGAGATGAG GTGGTTAAA AAACACAGCT GTACTAATTTC TTCACTTTCA	180
CAGAAAAGAG AAACTTGGGG GAGCAGCTCA CAGGAGAATT TACATAGAGC TGAGTCTGAA	240
TGTCCACCCC TAGAGAAGTT GAACCTCCCC CTGAGCTGTC TGTGCTCAGC AGGGGGCAGA	300
CAGCACATGG AGGGCGCAGG CCAGTCACAA GAGGAGCGCT GACTTAAACA GCTGTCTCC	360
CTTCCCAGNT GTTGNATTCT ACACACNATG TACATTGTTG TGCTTTATTG CTCCCACCCC	420
AGCCTCTGCC TGAAGCCCAG GGTGGAGGGA GGAACACCTG ACCAGATTC AGCTGGGTGG	480
GAGCACCAAG CCCCAATGG CTGGTGCTCT GTAAGNTTCT GAGGCTGCCA GGCTCNNGNC	540
ACTCGGAGCT GCAGACCAAG GGTACAGAGC CAGCCGACCA GCCAGCTCTT CTGAGGAGCA	600
GCAGAACAG AAGGATCAGT GCTGGACAAG ATGCAGGCTG GCTAGGAGCA GGCAGGGTGG	660
AAGGACGAGT GCAAGGCCAT GAGTCTGGGG CAGAGGGTTG TGCACATGGG GCTGTGGGG	720
CCTGCAGGGC ACCTCACGAG ACAGAACCAT TCTGTAGCAG AGCTTGACGG AGGAAGGGTG	780
TGAGGACCAC TGGCCTGGGG CCCCTTGGAG CACAGAGCTG CTTCCAGTTC ATCAGGGCT	840
GGCAGTGGCA GGCCCCAGCT CGGGCGTGT GCATTGGGAG ATTCAGGGAG AACCNCGAGG	900
CAGCCTGTGG GGCTGGGTGA GGAGGGAAGG CTGTGGTGGT ATCTTTGAGT NTGTCTTGGC	960
CGGGCCAGGG GTTAACACAG GATCAGTTGT TCTCAAAGAG TGAGAGCAGA TCATCACTGC	1020
TGTTTGTGGG GAGGTCAGGT GGACCCAGGT AGGAGAGTAG TTCATCAGGA TTGGTCAGTT	1080
CTGGGAGCAG ANCAGAGCT GGTTCTGAGG CCTCCCTGC CCCAGTCATG CTGGGAGGCC	1140
CCATCATGCC CGTGGCAGNA TTGAAAGCCA GTTCACTGAT GGGCCCTGTG TTTGGTTGGC	1200
CCAGGGGCTG CCTGGATGCA GGGGAAGGGT TTGGATGGTG TAGCTGGGTG CCTGGGGTGG	1260
GCCCGAGGTT GGGAGTGTGC AGTCCTGGTG GTCCAGGATT ATGGGCTGGG TCCCAGGTGA	1320
CCCTGCCTGG TGCCCATCCT GGCTGGGAG GCAAGGAGCA GACTTGNNNN GAGTCAGGAG	1380
GCTGCTGGGA ATGTCAGACT GGTAGGAGAT TGGGGTGGC CCCTGGGTG AACTCAGCAA	1440
GGTTTGGGGT GGCGGGTGTG GCAGATGGGA AAGATTCTGG GAAGGTTCCA GGCCCCCAGG	1500

AAGTTGGAAC CCTGGCTGGG NTAGTCGNTG GGGGTAGGGN CCNAAGGGGC TGCAATGGGG	1560
CAAANGGGCA GCGCCAGGGC CCAGGGCCGC AATCATCTCC ATCACACTGG GCATGAGCAC	1620
GTGGGCAGGG CTCACAGTAC GGCACTGCTT CAGCACTGGG CCCGTCCGGC TCCTCCTTGA	1680
TGTGTAGGTC AGGCTTCACA GGCACTGGTT TCCAGCTGCA TGTGGGGTCG ATGGTGATCT	1740
CCTCGTAGTC TGAGTTCTGA ATATAAATCA GGATGCCCTAG CATATACTGA TCCACCTCCA	1800
GGCCCTCCAG CAATGCCGTC TTGTTGCACA CCGGGACACC TCCAGGTCCC CCGCTCACAG	1860
TTAAAGCTGTA AGTATGACTC CAGGTCAAAG CACTGTATGT GGCGACAGTC GTGACCACGA	1920
GCTGGGAGCT GGATCCTGCG GAAGGTGATG GGGCACTTCA GGGACACCTT GATAGCCGTC	1980
TGCTCCACCC CATCCTCTCC ATTGGGCCA GGGGTGCCAG GGATGGTGCC GCTACTGAAG	2040
TTCCGCTTTA TCTTGGTGAT GCAGTGCTCA GCTGGCAAGN GGCGCTTCTT GAGGAGACCC	2100
TGCAGCACAG AGCGGACAGA CGGACGGTGC ACCAGCTGCA GCACGAAGAG GTGGGAGCAG	2160
CAGCAGGCGG TGACGGTGAT CTGGATGGTG TTGGCACCCG GCTGGCACAC ATGCTTCAGG	2220
TAGAGGGCT TGTGCGAGGT CTTGTTGTCT CCACGCTCGA TGCTGAGGGG TGTGNCATTG	2280
ACGCTGACCT GCACCGNNNGC CGGCCANTTG CTGGTTCATC TGCCGGTCCCT CGTGGTGGTA	2340
GCACTTGAAC TGCAGACTGA GCTCTAAGTC AGGTCTCAGC ATCAGGGTTT TATACACAGA	2400
GTCTCGNAGC TGGAAAGACAT GGTTGCTCAC AGCCAGGTTG TGCTGCAGGC GGAAGGGCTC	2460
CAGGACCACC CCATCCCGAA CTGGGAAGGT CAGGCGCAGC TCGTCACAGG GGACGCTTCC	2520
AGAGGGTGAT GGGTGCAAGG AGGCTGAGGC CTGGCTTGAG GTCAGGCAGG AAAGGAGACT	2580
TGACCTCCTG GCTTGGGGAC ACGTAGGGAG CACTGCTGCT AGGCGTCATG GGTGGTGTGG	2640
GATTCCCCGG CAGTGGGGAG CTGGGGTAAG CAGGGATGGA GCGGGAAAGGC CCACTCAAGC	2700
CAGGCTGGCT GTAGCTGATG CTGCCCCGT TGAANCTGGC CCCCTGCCCG TTGAACTGCT	2760
CTGTGGGCTT GTAATGCAGN CCTGTGGGGC CAGGGCAGA CAGGGACTGG GCCATGCCCT	2820
GCTGCAGGGG GAGTCTGTGT CCTGCGTAGG AGGAGGCAGG GCCAGGGGGC TGCCCGGGAC	2880
CAGGAGCATA CTGGGCAGTG CTGGCTGCAT ACTGGCCNNC TTGCAGATAT TGNTGN岑AG	2940
GATACACCTC TGAGTAGGTC TCTCTTGACC CNCTGTCAG GCAGCGGCTG CCCCTGGGA	3000
GGCCCAGGGT AGCCATGCTG AGGCAGTCGC TGTCCCTGCAT ACAAGGGTGT CATGCCTGCT	3060
GCCCGTGTAG GATTGATGGC CATGGAGGAA AGGCCTGAGG GGCCCATCAT TCCTCCCATG	3120
CCTGAAGGGT TCATGCCAGG GGGTACACTG GGCCCTCGAG GACCTCCATG CTGCAGAAC	3180
TGGCTGTTAA AAGATTGCCA AGTCCCCATC GCTCCATATT GGCTTAGCTT CCTGGCTCTN	3240
CTTCTCTTGC AGGGNNGCCA CAGTAGCTGT GGCTGTGGCT GTGGCGTN C TGCAGCAGCA	3300
GCCATGGCAG CTGCAGCTCT GCTTGTGTGA AGTCAG	3336

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1494 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HW088

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 9..686

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: complement (612..909)
 (D) OTHER INFORMATION: /label= SAC_24336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GTCGACCC GCT GCG GTC TAT CTG GGC AGC ACC ATG CTC GCG CTC CGA AGC	50
Ala Ala Val Tyr Leu Gly Ser Thr Met Leu Ala Leu Arg Ser	
1 5 10	
GGC CTG AGG ACG GCG CTG GCC CCG CGG GCT CTG ACG CCT CAG GTA TGT	98
Gly Leu Arg Thr Ala Leu Ala Pro Arg Ala Leu Thr Pro Gln Val Cys	
15 20 25 30	
TCA CCT TTT GCT ACA GGC CCC AGG CAA AGC GAT GGG ACA TTG TAT GAA	146
Ser Pro Phe Ala Thr Gly Pro Arg Gln Ser Asp Gly Thr Leu Tyr Glu	
35 40 45	
TTC CGC ACC TAC TCT CTG AAG CCC TCA AAG ACA AAT GCG TTC CTG CAG	194
Phe Arg Thr Tyr Ser Leu Lys Pro Ser Lys Thr Asn Ala Phe Leu Gln	
50 55 60	
AAT TTT CAG AAA TAC GTT CAC CTT CGG ACA GCT CAC TCT GAG ATG ATT	242
Asn Phe Gln Lys Tyr Val His Leu Arg Thr Ala His Ser Glu Met Ile	
65 70 75	
GGA TAC TGG ACC GTA GAA TTT GGA GGC AAA ATA AAC AGA GTG TTC CAT	290
Gly Tyr Trp Thr Val Glu Phe Gly Gly Lys Ile Asn Arg Val Phe His	
80 85 90	
ATT TGG AAG TAT GAT AAT TTT GCT CAT CGA ACT GCC GTC CGC AAA GCC	338
Ile Trp Lys Tyr Asp Asn Phe Ala His Arg Thr Ala Val Arg Lys Ala	
95 100 105 110	
TTG GCC AAG GAT AAG GAA TGG CAA GAA CAA TTC CTC ATT TCA AAT TTG	386
Leu Ala Lys Asp Lys Glu Trp Gln Glu Gln Phe Leu Ile Ser Asn Leu	
115 120 125	
GCT TTC ATG GAT GAA CAA GAG GTT GAG ATT ACC TAC TTG GTA CCC TGG	434
Ala Phe Met Asp Glu Gln Glu Val Glu Ile Thr Tyr Leu Val Pro Trp	
130 135 140	

TGT AAA ATA AGA ACA CCT CCC AAG GAA GGA GTC TAT GAA CTG GCT ACC Cys Lys Ile Arg Thr Pro Pro Lys Glu Gly Val Tyr Glu Leu Ala Thr 145 150 155	482
TTT CAG ATG AAG CCT GGT GGC CCA GCT CTA TGG GGT GAT GCA TTC AAA Phe Gln Met Lys Pro Gly Gly Pro Ala Leu Trp Gly Asp Ala Phe Lys 160 165 170	530
AGG GCA ATA AAC GCC CAT GTT GAG CTT GGC TAC TCT ACA CTA GTT GGT Arg Ala Ile Asn Ala His Val Glu Leu Gly Tyr Ser Thr Leu Val Gly 175 180 185 190	578
GTT TTC CAC ACT GAA TAT GGA GCC CTC AAC AGA GTT CGG GAA AGT GTC Val Phe His Thr Glu Tyr Gly Ala Leu Asn Arg Val Arg Glu Ser Val 195 200 205	626
AAT TAC CTC GAG TCT CAG CAG AAT ATG TTC CTG ATT CCA ACC TCA TTT Asn Tyr Leu Glu Ser Gln Gln Asn Met Phe Leu Ile Pro Thr Ser Phe 210 215 220	674
TCA CCA TTG AAG TAGTTCCCTA CCGAGCGCTG AGCATTCCCA TCACGGAGGT Ser Pro Leu Lys 225	726
GAGATGCGTT TCCCCCAGAC AATGCCCTG TTCATTGTCT GAAGGAGGTG CTGAGCTACC GCACGTGCCCT CTGCATGTCT GAGACTTCAT GTATCCTTTA CTACCAAGTCG CTCAGGAAAT GTTTCTGTCC CTTTTCATGT CTACTGGATG TCAGAAAAGTG GTGTTATTAC TCCATGCCCT GGTACTTCAT TGTTCTTCTG TGGTTTTATG ATTAAGTCTT GTCCCTAAAA TATGATTTTG AAATTTTTTC CCTCAAAATA TTTGGAAATT AAATAAAATAC AATATCTGCC TTTTTATTGC GTTCATTTTC CCTGAAATT TTAACTGTTT TTACCAAGTAA TGTTTACTTT GTGATTTCAA ATGGGATTGA TAGAAGTCAG AGAAAGAACT GGAAGAGCTT GAAGGGGCTC GAGACCCAT ATGTACAACA ATGCCAAGCA ACCAGAGCTT CCAGGGACTA AGCCACTACC TAAAGACTAT ACATGGACTG ACCCTGGACT CTGACCTCAT AGGTAGCAAT GAATATCCTA GTAAGAGCAC CAGTGGAAAGG GGAAGCCCTG GGTCTGCTA AGACTGAACC CCAGTGAACG TGATTGTTGT GGGGAGAGTG GTAATGGGGG GAGGATGGGG AGGGGAAGCC CATATAGAAG GGGAGGGAGA GGGGTTAGGG GGATGTCGGC CCAGAAACCA GGAAGGGGAA TAACAATTGA AATGTAAATA AGAAATACTC AAGTTAATAA AGATGGAGAA AAGAAAAAGA AAGTCGAC	786 846 906 966 1026 1086 1146 1206 1266 1326 1386 1446 1494

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 226 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Ala Ala Val Tyr Leu Gly Ser Thr Met Leu Ala Leu Arg Ser Gly Leu
 1 5 10 15

Arg Thr Ala Leu Ala Pro Arg Ala Leu Thr Pro Gln Val Cys Ser Pro
 20 25 30

Phe Ala Thr Gly Pro Arg Gln Ser Asp Gly Thr Leu Tyr Glu Phe Arg
 35 40 45

Thr Tyr Ser Leu Lys Pro Ser Lys Thr Asn Ala Phe Leu Gln Asn Phe
 50 55 60

Gln Lys Tyr Val His Leu Arg Thr Ala His Ser Glu Met Ile Gly Tyr
 65 70 75 80

Trp Thr Val Glu Phe Gly Gly Lys Ile Asn Arg Val Phe His Ile Trp
 85 90 95

Lys Tyr Asp Asn Phe Ala His Arg Thr Ala Val Arg Lys Ala Leu Ala
 100 105 110

Lys Asp Lys Glu Trp Gln Glu Gln Phe Leu Ile Ser Asn Leu Ala Phe
 115 120 125

Met Asp Glu Gln Glu Val Glu Ile Thr Tyr Leu Val Pro Trp Cys Lys
 130 135 140

Ile Arg Thr Pro Pro Lys Glu Gly Val Tyr Glu Leu Ala Thr Phe Gln
 145 150 155 160

Met Lys Pro Gly Gly Pro Ala Leu Trp Gly Asp Ala Phe Lys Arg Ala
 165 170 175

Ile Asn Ala His Val Glu Leu Gly Tyr Ser Thr Leu Val Gly Val Phe
 180 185 190

His Thr Glu Tyr Gly Ala Leu Asn Arg Val Arg Glu Ser Val Asn Tyr
 195 200 205

Leu Glu Ser Gln Gln Asn Met Phe Leu Ile Pro Thr Ser Phe Ser Pro
 210 215 220

Leu Lys
 225

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HW089

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 8..1006

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION: 961..1076
 (D) OTHER INFORMATION: /label= SAC_24461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GTGCGACC AAG CAA CAG CAG GGA AGT GAA TTT CAG ACA CTG CTG GAG GCT Lys Gln Gln Gln Gly Ser Glu Phe Gln Thr Leu Leu Glu Ala 1 5 10	49
GAG GAG ACC AAA GCC GCC TCT GAC GCT TCA AAT AAA AAG CTT TGG TCC Glu Glu Thr Lys Ala Ala Ser Asp Ala Ser Asn Lys Lys Leu Trp Ser 15 20 25 30	97
CTC AGA ACT CTA CCC TTC CAG CCC TGC TCT GAA GCC TCA GAC GTG AGA Leu Arg Thr Leu Pro Phe Gln Pro Cys Ser Glu Ala Ser Asp Val Arg 35 40 45	145
ACC ATG TCT GTG ACC CTG CAA GCT GTC CTC TAC AGT CTT CAG GAG GAG Thr Met Ser Val Thr Leu Gln Ala Val Leu Tyr Ser Leu Gln Glu Glu 50 55 60	193
CAG TCC AGG CTC AAG ACG AGG CTG CAG GAA CTA CAG CAG CTG AAA AGG Gln Ser Arg Leu Lys Thr Arg Leu Gln Glu Leu Gln Gln Leu Lys Arg 65 70 75	241
GAG CGC ATA GAT GTT CCC AGA GAC AAG ATC CCA TTC CCG GTG CCT GAA Glu Arg Ile Asp Val Pro Arg Asp Lys Ile Pro Phe Pro Val Pro Glu 80 85 90	289
GTC CCC GTG GTA TTC CAA GGT CTA ACT AAG CAG AGC GGC CAA GCA CCC Val Pro Val Val Phe Gln Gly Leu Thr Lys Gln Ser Gly Gln Ala Pro 95 100 105 110	337
AAG TCT CTA GTT TCT AAC TTG AAG ATC TGC TGC CCT CTG CCT GGA GGT Lys Ser Leu Val Ser Asn Leu Lys Ile Cys Cys Pro Leu Pro Gly Gly 115 120 125	385
TCT GCT CTG ATC ACC TTT GAT GAC CCC AAA GTG GTT GAG CGG TTG CTA Ser Ala Leu Ile Thr Phe Asp Asp Pro Lys Val Val Glu Arg Leu Leu 130 135 140	433
CAA CAA AAG GAA CAT AAA GTT GAC ATC GAG GAC TGC CGG CTG CGG GTG Gln Gln Lys Glu His Lys Val Asp Ile Glu Asp Cys Arg Leu Arg Val 145 150 155	481
CAG ATC CAG CCC TTG GAG CTG CCT ATG GTG ACC AAC ATC CAG GTG TCC Gln Ile Gln Pro Leu Glu Leu Pro Met Val Thr Asn Ile Gln Val Ser 160 165 170	529
AGC CAG CCG GAT AGC CAC AGG GTG CTA GTC AGT GGC TTT CCT ACT GGA Ser Gln Pro Asp Ser His Arg Val Leu Val Ser Gly Phe Pro Thr Gly 175 180 185 190	577
CTT AGG CTG AGT GAG GAG GAG CTA CTG GAC AAG TTA GAG ATC TTC TTC Leu Arg Leu Ser Glu Glu Leu Leu Asp Lys Leu Glu Ile Phe Phe 195 200 205	625
GGC AAG GCC AAG AAT GGA GGT GGG GAT GTG GAG ACC CGG GAG ATG CTG	673

Gly Lys Ala Lys Asn Gly Gly Asp Val Glu Thr Arg Glu Met Leu			
210	215	220	
CAA GGG ACT GTC ATG CTG GGA TTT GCT AAT GAA GAA GTG GCC CAG CAC			721
Gln Gly Thr Val Met Leu Gly Phe Ala Asn Glu Glu Val Ala Gln His			
225	230	235	
TTA TGC CAG ATT GGC CAG TTC AGA GTC CCA CTG GGT CGG CAG CAG GTC			769
Leu Cys Gln Ile Gly Gln Phe Arg Val Pro Leu Gly Arg Gln Gln Val			
240	245	250	
CTT TTG AGG GTC TCT CCC TAT GTG AGT GGG GAG ATC CAG GAA GCT GAG			817
Leu Leu Arg Val Ser Pro Tyr Val Ser Gly Glu Ile Gln Glu Ala Glu			
255	260	265	270
ATC AAA TTC CAG CAA GCA CCT CAT TCA GTG CTG GTG ACG AAT ATT CCC			865
Ile Lys Phe Gln Gln Ala Pro His Ser Val Leu Val Thr Asn Ile Pro			
275	280	285	
GAC GTC CTG GAT GTG CAG GAA CTG CAT GAC ATT CTG GAG ATC CAC TTC			913
Asp Val Leu Asp Val Gln Glu Leu His Asp Ile Leu Glu Ile His Phe			
290	295	300	
CAG AAG CCT ACC CGT GGG GGC GGA GAG GTG GAG GCC CTG GCA GTT GTA			961
Gln Lys Pro Thr Arg Gly Gly Glu Val Glu Ala Leu Ala Val Val			
305	310	315	
CCT GTG GGG CAG CAG GGC CTG GCT GTC TTT ACT TCT GAG TCA AGC			1006
Pro Val Gly Gln Gly Leu Ala Val Phe Thr Ser Glu Ser Ser			
320	325	330	
TAGGGCTGCA TGTCCACCTG CTGGGCATGG GACTGCTCAT TGCCTAATGC TACCAAGAAC			1066
AGTGAAAGGC GTCGAC			1082

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Lys	Gln	Gln	Gln	Gly	Ser	Glu	Phe	Gln	Thr	Leu	Leu	Glu	Ala	Glu	Glu
1					5					10			15		
Thr	Lys	Ala	Ala	Ser	Asp	Ala	Ser	Asn	Lys	Lys	Leu	Trp	Ser	Leu	Arg
					20			25				30			
Thr	Leu	Pro	Phe	Gln	Pro	Cys	Ser	Glu	Ala	Ser	Asp	Val	Arg	Thr	Met
					35		40				45				
Ser	Val	Thr	Leu	Gln	Ala	Val	Leu	Tyr	Ser	Leu	Gln	Glu	Gln	Ser	
					50		55			60					
Arg	Leu	Lys	Thr	Arg	Leu	Gln	Glu	Leu	Gln	Gln	Leu	Lys	Arg	Glu	Arg
					65		70		75		80				
Ile	Asp	Val	Pro	Arg	Asp	Lys	Ile	Pro	Phe	Pro	Val	Pro	Glu	Val	Pro

WO 98/53071

90

95

85

Val Val Phe Gln Gly Leu Thr Lys Gln Ser Gly Gln Ala Pro Lys Ser	110
100	105
Leu Val Ser Asn Leu Lys Ile Cys Cys Pro Leu Pro Gly Gly Ser Ala	125
115	120
Leu Ile Thr Phe Asp Asp Pro Lys Val Val Glu Arg Leu Leu Gln Gln	140
130	135
Lys Glu His Lys Val Asp Ile Glu Asp Cys Arg Leu Arg Val Gln Ile	160
145	150
Gln Pro Leu Glu Leu Pro Met Val Thr Asn Ile Gln Val Ser Ser Gln	175
165	170
Pro Asp Ser His Arg Val Leu Val Ser Gly Phe Pro Thr Gly Leu Arg	190
180	185
Leu Ser Glu Glu Glu Leu Leu Asp Lys Leu Glu Ile Phe Phe Gly Lys	205
195	200
Ala Lys Asn Gly Gly Asp Val Glu Thr Arg Glu Met Leu Gln Gly	220
210	215
Thr Val Met Leu Gly Phe Ala Asn Glu Val Ala Gln His Leu Cys	240
225	230
Gln Ile Gly Gln Phe Arg Val Pro Leu Gly Arg Gln Gln Val Leu Leu	255
245	250
Arg Val Ser Pro Tyr Val Ser Gly Glu Ile Gln Glu Ala Glu Ile Lys	270
260	265
Phe Gln Gln Ala Pro His Ser Val Leu Val Thr Asn Ile Pro Asp Val	285
275	280
Leu Asp Val Gln Glu Leu His Asp Ile Leu Glu Ile His Phe Gln Lys	300
290	295
Pro Thr Arg Gly Gly Glu Val Glu Ala Leu Ala Val Val Pro Val	320
305	310
Gly Gln Gln Gly Leu Ala Val Phe Thr Ser Glu Ser Ser	330
325	

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2263 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: HW090

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 335..937

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1355..1434
 (D) OTHER INFORMATION: /label= SAC_24197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GTGACCTTT AAGCTTACCA TCAGAACAAAC AAATCAAAT GTAAACTTAA AATATAACCA	60
AAAGAGGGAC AGCTCTTAG GAAAAGAAA AAACCTTAA TAGTGAATAA ACAACTACAA	120
CCACTTAACC ATTGTAGGCT TAAAAGCAGC CATCAATAAA GAAAGCGTTC AAGCTCAACA	180
TACACACACA CACACACACA CACACACGCT CCCTCCCTCC GGCGCTCTAC TCCGCGCCCG	240
CCCGCCCGCT CGCCCGCCCG CCCGCCTCGC ACGCACCGGC CTCGGCTCCC CGCGCCCGCC	300
GCCGAGCGAA GCTGCTCTGG GATCGGAGCA GCTC ATG GAG AAA GTG CCG GGC Met Glu Lys Val Pro Gly	352
1 5	
GAC ATG GAG ATA GAG CGC AGG GAG AGG AAC GAG GAG CTG TCC GAG GCG Asp Met Glu Ile Glu Arg Arg Glu Arg Asn Glu Glu Leu Ser Glu Ala	400
10 15 20	
GAG AGG AAG GCG GTT CAG GCT ACG TGG GCC CGG CTG TAT GCC AAC TGC Glu Arg Lys Ala Val Gln Ala Thr Trp Ala Arg Leu Tyr Ala Asn Cys	448
25 30 35	
GAG GAC GTG GGG GTG GCC ATC CTG GTG AGG TTC TTT GTG AAC TTC CCG Glu Asp Val Gly Val Ala Ile Leu Val Arg Phe Phe Val Asn Phe Pro	496
40 45 50	
TCG GCC AAG CAG TAC TTC AGC CAG TTT AAA CAC ATG GAG GAT CCG TTG Ser Ala Lys Gln Tyr Phe Ser Gln Phe Lys His Met Glu Asp Pro Leu	544
55 60 65 70	
GAG ATG GAG AGG AGT CCT CAG CTG CGG AAA CAT GCC TGC CGG GTC ATG Glu Met Glu Arg Ser Pro Gln Leu Arg Lys His Ala Cys Arg Val Met	592
75 80 85	
GGG GCC CTC AAC ACG GTC GTG GAG AAC CTG CAT GAC CCA GAC AAG GTA Gly Ala Leu Asn Thr Val Val Glu Asn Leu His Asp Pro Asp Lys Val	640
90 95 100	
TCC TCT GTG CTC GCG CTG GTT GGC AAG GCC CAC GCC CTC AAG CAC AAG Ser Ser Val Leu Ala Leu Val Gly Lys Ala His Ala Leu Lys His Lys	688
105 110 115	
GTG GAA CCT ATG TAC TTT AAG ATT CTC TCT GGG GTC ATT CTG GAC GTG Val Glu Pro Met Tyr Phe Lys Ile Leu Ser Gly Val Ile Leu Asp Val	736
120 125 130	
ATC GCC GAG GAG TTT GCC AAT GAC TTC CCC GTC GAG ACG CAG AAA GCC Ile Ala Glu Glu Phe Ala Asn Asp Phe Pro Val Glu Thr Gln Lys Ala	784
135 140 145 150	
TGG ACC AAG CTG CGC GGT CTC ATC TAC AGC CAT GTG ACC GCG GCC TAC	832

Trp Thr Lys Leu Arg Gly Leu Ile Tyr Ser His Val Thr Ala Ala Tyr		
155	160	165
AAG GAA GTG GGC TGG GTA CAG CAG CCT ACC AGC CAC ACT GCC CTC TTC		880
Lys Glu Val Gly Trp Val Gln Gln Pro Thr Ser His Thr Ala Leu Phe		
170	175	180
AGG GCC ATA GGA CCC CTC CCA GCT CCC CCC TCC CTG GCA GCA CTT TGG		928
Arg Ala Ile Gly Pro Leu Pro Ala Pro Ser Leu Ala Ala Leu Trp		
185	190	195
GCA GAA GGC TGACTTCTGA AGACACTCCT TGACCTTCCA TTTCTGGGTG		977
Ala Glu Gly		
200		
CCAAGGAAGC TGGAGGAACC CCTGACTTGA CTTCCCAGAA GGAGGCCTTC ATCATGGCTG		1037
TGGTCTCCCA CGTTACTGGG AGGTGGGGCT GGCTACCTGG ATGCTGAATT TAGCAGAGGG		1097
GAACCCCTCT GCCTCGCAGC AGAGGGCACA CCCTCCTTAG CTTTCACTGT CAAGAGAGGG		1157
ACCTGGCATG TGGCCGGTGG GAAGCAAGGA CAAGCCTTG AGTCACTTCA GAAAGGAAC		1217
AGCCCTGCTT CACTCTGCCA TACAGCATG CAGGTTCTCC TCACCATCTC TGAGCATTGC		1277
GCACACACAC GTCTACCATA TACACAGATA TATTCTATAT ACGAGCTCTA TATAAAATA		1337
TATACACACA CACACGTACA TATCTGTCGC GTGCACCTGC AGGCCCCAGAA GCCTAGGCCT		1397
CGCACAGCTG TGGGAGACCC GGAAGAGTCC TGGCCGTACT TCAGGGCAGC TCTACCGGGA		1457
GCAGGGAGAA AGCTTGCAAC AGCACGAGAG GGCGGGGGCG GGTGGGAGAG TCGGGGTGAC		1517
TCAGCTCACC CCGCACAGCT CAGTGCCTG CAATCTCCC CTTCCGCCCC CCAAAAGAGA		1577
ACACTTGGTT TGCCCGGTGT CGGGGCGCAC ACCTGTAATC CCCGAGTTG GGACGCAGAG		1637
GAAGGACAAT CTTTGCAAGT CTGAGGTCA GTGGTCTACA CTTGGTCTCC ATCTTGGTGA		1697
GTTCGGGCT AGCTGGGTC GACTCAGGGA GACCCCGTGT CAAACAAAAC AAGAACGAA		1757
GAGAAGATCT GGCTCCCCCTC CCCTCCCCAA GGGTTGCCC GACTGACTTG CTCCGGAAAG		1817
GGGCACACCG AGAATTCAAG AGACCCAGT GGGGTGCTGG CCAGTGTAGG TGTCCGGCGT		1877
TTGGGGTGG GGTGAGGGGC AGCTTCAGCG TGGAGCCCTA GAATGTCAGC CTCACCCGCT		1937
CACTTCAGAC AGCAGCCAGG CCACAGGACC AGGGGCCATA CTCAAACCCC TCAGCAGAGA		1997
CCAGGGCGCC TCTCTCCTGC CCTCCTCGGG GCCACCTGCC CATCCTCTCC AACTAGTCTC		2057
CGTAAACATTC GCTGGGGACC CCGTGTGTAC CCCTTGGTCA CGTGTACTGT CCTGGAGGAC		2117
GTCTTACTGC TGTGGCTACC GTGCCTGCGT CCCCTCTGGT CCCACCCCTCA CGCAGCCTTC		2177
CTGTAACCTGC CTGTCTTTTT GTAGTTCTG ATGTTGTAA CCAGACCCAG CTGTGTCATT		2237
AAACAGGTCT GTTCTTCCTG TAAAAAA		2263

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Met	Glu	Lys	Val	Pro	Gly	Asp	Met	Glu	Ile	Glu	Arg	Arg	Glu	Arg	Asn	
1							5							10		15
Glu Glu Leu Ser Glu Ala Glu Arg Lys Ala Val Gln Ala Thr Trp Ala																
								20		25				30		
Arg Leu Tyr Ala Asn Cys Glu Asp Val Gly Val Ala Ile Leu Val Arg																
								35		40				45		
Phe Phe Val Asn Phe Pro Ser Ala Lys Gln Tyr Phe Ser Gln Phe Lys																
								50		55				60		
His Met Glu Asp Pro Leu Glu Met Glu Arg Ser Pro Gln Leu Arg Lys																
								65		70				75		80
His Ala Cys Arg Val Met Gly Ala Leu Asn Thr Val Val Glu Asn Leu																
								85		90				95		
His Asp Pro Asp Lys Val Ser Ser Val Leu Ala Leu Val Gly Lys Ala																
								100		105				110		
His Ala Leu Lys His Lys Val Glu Pro Met Tyr Phe Lys Ile Leu Ser																
								115		120				125		
Gly Val Ile Leu Asp Val Ile Ala Glu Glu Phe Ala Asn Asp Phe Pro																
								130		135				140		
Val Glu Thr Gln Lys Ala Trp Thr Lys Leu Arg Gly Leu Ile Tyr Ser																
								145		150				155		160
His Val Thr Ala Ala Tyr Lys Glu Val Gly Trp Val Gln Gln Pro Thr																
								165		170				175		
Ser His Thr Ala Leu Phe Arg Ala Ile Gly Pro Leu Pro Ala Pro Pro																
								180		185				190		
Ser Leu Ala Ala Leu Trp Ala Glu Gly																
								195		200						

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1740 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HW092

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: complement (303..566)
- (D) OTHER INFORMATION: /label= SAC_24320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GTCGACCTCG GAGCTGGGGA CCGAACCCAG GGCCCTTGC	60
CACTGAGCTA AATCCCCAAC CCCTAGCCCT TTGT	120
GGTTGGCCTT AAATTCCCTGA TCCTCC	180
GGCCATCACA CTGTTTATCC AGTGCTGAAT CAAACCCAGA ATCTTCCACA TGCTAGGCGA	240
GCAGTCTCCT AAATACTACA CGGCTATAGG TTCAGCCTAG ATCTCTCTTT TGAAGCTCTC	300
GTACACCTAT AGGGGCCACT AATCCTAAAG ACGCAGAGGA TGAAAACCAC CAGGCCAAG	360
GGTTAACGTG GAAAACAGAG CCCTGGTGT	420
CACAGTCATC ACCCAGATTCTGAAA TAGCGGCTTC TTGTTTAGAA CGGAACCGCA	480
CCTGCTGGAA TACGTGTCAA CAAACAATCG CTTTGT	540
AGGCAATGGG ACTTCCTGAA GCGAGTACTG GAAGACTTAT TCTT	600
CTCATTTAA CACGAGGCTC AGGGGCCAG TGCTGGCCAT CTTCC	660
TCCCTGGTGT TCATCTTATT TGGTTTCAA CAGGTTTATT TCCATTGCAG CCCGGGCTT	720
CCAACGCCA AAAACGCCA GCCCACGATG CCGTAAATGG TGAGCAGC	780
TCCTCTCCCT GAGAACCCAG ACCCTTGTT GTTCCGCCAT TCCAAAAGGC CCTGGGAAGG	840
TTCTTGTGTC CTC	900
TCTCGCTCCT GGCTAAATCT TTCTGCTTGT TCTT	960
TACTACTTT CCTGATGCAG TCTGACGAAC GTCTGTTGAA CACATGGGA CAGTTTAAAC	1020
AGGAGTTATT TTGGTGGCAA AGGCAGTCAG TTGTGATTAA AAGTGT	1080
TCCAAGGTTG TCTCCATGGA CTCCGAAAT AACCA	1140
GAATATGAGA GGCAGATAGC ACCTATTACTG GGGTGCAGCC GGGCTCCAGA	1200
TTAATGGGG CAAGCAAAGG TCCAGGCC	1260
AGACATGGCC AATT	1320
TTAGTGTGAT AAGTATTCAA TAAGGGCTTG GAATCTAATT ATTTGTAAGA AGTGTCTTG	1380
TTTCCTGATC TGTAAGGAG ATGGGAAAT ACTGTGATTG CGTGC	1440
AAAAAGCAA CATAAAAAAA TGCAAATACA GAAGAAAAGA TGTGGGTTT GAAGTGGCT	1500
TTAGAGAGCT GTGTAACCTT GGGGAAGTCA CCTCGTCTCT CTGTGACTTG AATT	1560
CAACAATAAT GCTGGGGGAC AAGGTGCTCT CCAAATTCCC CTTCA	1620
GATAACTATC CCAGATAGAT CCAAAC	1680
CAGATAACAC GGACTTGAAA CTTAGTCAC CTGATATTTC TTAATGACTT AACACCAC	

TACCTCACCC CAGAGCTAGC CTGTCCCCCTG TGTGCCACC AGTAACCTTG AAATGTCGAC 1740

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HW093

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 8..1385

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 798..1385
- (D) OTHER INFORMATION: /label= SAC_24538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GTCGACT CTG CCT CAG CCG CTG CCG CCA CTG CTG CTG CAG GAT CCG		49
Leu Pro Gln Pro Leu Pro Pro Pro Leu Leu Leu Gln Asp Pro		
1 5 10		
CCG CAG CCA CCA GTC TCG CGC GTC GTC GCT CCC TCC TTG GAC AGT AAT		97
Pro Gln Pro Pro Val Ser Arg Val Val Ala Pro Ser Leu Asp Ser Asn		
15 20 25 30		
TTT ATG AAT AAG CAT CAG AAG CCG GTA CTA ACA GGC CAG CGG TTC AAA		145
Phe Met Asn Lys His Gln Lys Pro Val Leu Thr Gly Gln Arg Phe Lys		
35 40 45		
ACC CGG AAA AGG GAT GAA AAA GAG AAA TTC GAA CCC ACA GTC TTC AGG		193
Thr Arg Lys Arg Asp Glu Lys Glu Lys Phe Glu Pro Thr Val Phe Arg		
50 55 60		
GAT ACA CTT GTC CAG GGG CTT AAT GAA GCT GGT GAT GAC CTT GAA GCT		241
Asp Thr Leu Val Gln Gly Leu Asn Glu Ala Gly Asp Asp Leu Glu Ala		
65 70 75		
GTA GCC AAA TTC TTG GAC TCT ACT GGC TCA CGA CTA GAT TAT CGT CGC		289
Val Ala Lys Phe Leu Asp Ser Thr Gly Ser Arg Leu Asp Tyr Arg Arg		
80 85 90		
TAT GCA GAC ACA CTC TTT GAT ATC CTG GTG GCT GGC AGC ATG CTT GCC		337
Tyr Ala Asp Thr Leu Phe Asp Ile Leu Val Ala Gly Ser Met Leu Ala		
95 100 105 110		
CCT GGA GGA ACA CGC ATA GAT GAT GGT GAC AAG ACC AAG ATG ACC AAC		385
Pro Gly Gly Thr Arg Ile Asp Asp Gly Asp Lys Thr Lys Met Thr Asn		
115 120 125		

CAC TGT GTG TTT TCA GCA AAT GAA GAT CAT GAA ACC ATC CGA AAC TAT His Cys Val Phe Ser Ala Asn Glu Asp His Glu Thr Ile Arg Asn Tyr 130 135 140	433
GCT CAG GTC TTC AAC AAA CTC ATC AGG AGA TAC AAA TAT TTG GAA AAG Ala Gln Val Phe Asn Lys Leu Ile Arg Arg Tyr Lys Tyr Leu Glu Lys 145 150 155	481
GCA TTT GAA GAT GAA ATG AAA AAG CTT CTC CTC TTC CTT AAA GCA TTT Ala Phe Glu Asp Glu Met Lys Lys Leu Leu Leu Phe Leu Lys Ala Phe 160 165 170	529
TCT GAA GCA GAG CAG ACA AAG TTG GCA ATG CTG TCT GGG ATC CTG TTG Ser Glu Ala Glu Gln Thr Lys Leu Ala Met Leu Ser Gly Ile Leu Leu 175 180 185 190	577
GGC AAT GGA ACC CTC CCG GCC ACC ATC CTT ACC AGT CTC TTC ACC GAC Gly Asn Gly Thr Leu Pro Ala Thr Ile Leu Thr Ser Leu Phe Thr Asp 195 200 205	625
AGC TTA GTC AAA GAA GGC ATC GCA GCC TCG TTC GCT GTC AAG CTT TTC Ser Leu Val Lys Glu Gly Ile Ala Ala Ser Phe Ala Val Lys Leu Phe 210 215 220	673
AAA GCC TGG ATG GCA GAG AAA GAT GCC AAT TCT GTC ACC TCT TCA TTG Lys Ala Trp Met Ala Glu Lys Asp Ala Asn Ser Val Thr Ser Ser Leu 225 230 235	721
AGA AAA GCC AAC CTG GAC AAG AGG CTG CTT GAA CTC TTC CCA GTG AAC Arg Lys Ala Asn Leu Asp Lys Arg Leu Leu Glu Leu Phe Pro Val Asn 240 245 250	769
AGA CAG AGT GTG GAT CAT TTC GCC AAG TAC TTC ACT GAC GCA GGA CTG Arg Gln Ser Val Asp His Phe Ala Lys Tyr Phe Thr Asp Ala Gly Leu 255 260 265 270	817
AAG GAG CTG TCA GAC TTT CTC CGA GTC CAG CAG TCA CTG GGC ACC AGG Lys Glu Leu Ser Asp Phe Leu Arg Val Gln Gln Ser Leu Gly Thr Arg 275 280 285	865
AAG GAA CTG CAG AAG GAG CTG CAA GAG CGA CTG TCT CAG GAA TGC CCC Lys Glu Leu Gln Lys Glu Leu Gln Glu Arg Leu Ser Gln Glu Cys Pro 290 295 300	913
ATC AAG GAG GTG GTG CTT TAC GTC AAA GAG GAA ATG AAA AGG AAC GAC Ile Lys Glu Val Val Leu Tyr Val Lys Glu Glu Met Lys Arg Asn Asp 305 310 315	961
CTT CCG GAG ACA GCT GTG ATC GGG CTG CTG TGG ACC TGC GTC ATG AAC Leu Pro Glu Thr Ala Val Ile Gly Leu Leu Trp Thr Cys Val Met Asn 320 325 330	1009
GCT GTG GAA TGG AAC AAG AAG GAG GAG CTG GTT GCT GAG CAG GCT CTT Ala Val Glu Trp Asn Lys Lys Glu Glu Leu Val Ala Glu Gln Ala Leu 335 340 345 350	1057
AAG CAC CTG AAG CAA TAC GCT CCC CTG GCC GTG TTC AGT TCC CAA Lys His Leu Lys Gln Tyr Ala Pro Leu Leu Ala Val Phe Ser Ser Gln 355 360 365	1105
GGC CAG TCA GAG CTT GTC CTC CTG CAG AAG GTT CAG GAA TAC TGC TAT Gly Gln Ser Glu Leu Val Leu Gln Lys Val Gln Glu Tyr Cys Tyr	1153

370	375	380	
GAC AAC ATC CAC TTC ATG AAA GCC TTC CAG AAG ATC GTG GTT CTC TTT Asp Asn Ile His Phe Met Lys Ala Phe Gln Lys Ile Val Val Leu Phe			1201
385	390	395	
TAT AAA GCC GAC GTT CTG AGC GAG GAG GCG ATA CTG AAG TGG TAT AAA Tyr Lys Ala Asp Val Leu Ser Glu Glu Ala Ile Leu Lys Trp Tyr Lys			1249
400	405	410	
GAA GCA CAT GCC GCC AAA GGC AAA AGC GTC TTC CTT GAC CAG ATG AAG Glu Ala His Ala Ala Lys Gly Lys Ser Val Phe Leu Asp Gln Met Lys			1297
415	420	425	430
AAA TTT GTG GAG TGG TTA CAA AAT GCA GAA GAA GAA TCT GAA TCA GAA Lys Phe Val Glu Trp Leu Gln Asn Ala Glu Glu Glu Ser Glu Ser Glu			1345
435	440	445	
GGT GAA GAA AGC TAAATGTCTC CAGCACACTG CCTAAAAA Gly Glu Glu Ser			1385
450			

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - ii) MOLECULE TYPE: protein
 - xii) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Leu	Pro	Gln	Pro	Leu	Pro	Pro	Pro	Leu	Leu	Leu	Gln	Asp	Pro	Pro	Gln
1				5					10					15	
Pro	Pro	Val	Ser	Arg	Val	Val	Ala	Pro	Ser	Leu	Asp	Ser	Asn	Phe	Met
		20						25					30		
Asn	Lys	His	Gln	Lys	Pro	Val	Leu	Thr	Gly	Gln	Arg	Phe	Lys	Thr	Arg
		35					40				45				
Lys	Arg	Asp	Glu	Lys	Glu	Lys	Phe	Glu	Pro	Thr	Val	Phe	Arg	Asp	Thr
		50			55					60					
Leu	Val	Gln	Gly	Leu	Asn	Glu	Ala	Gly	Asp	Asp	Leu	Glu	Ala	Val	Ala
		65			70				75				80		
Lys	Phe	Leu	Asp	Ser	Thr	Gly	Ser	Arg	Leu	Asp	Tyr	Arg	Arg	Tyr	Ala
		85					90				95				
Asp	Thr	Leu	Phe	Asp	Ile	Leu	Val	Ala	Gly	Ser	Met	Leu	Ala	Pro	Gly
		100					105					110			
Gly	Thr	Arg	Ile	Asp	Asp	Gly	Asp	Lys	Thr	Lys	Met	Thr	Asn	His	Cys
		115				120					125				
Val	Phe	Ser	Ala	Asn	Glu	Asp	His	Glu	Thr	Ile	Arg	Asn	Tyr	Ala	Gln
		130			135					140					
Val	Phe	Asn	Lys	Leu	Ile	Arg	Arg	Tyr	Lys	Tyr	Leu	Glu	Lys	Ala	Phe
		145			150				155				160		

Glu Asp Glu Met Lys Lys Leu Leu Leu Phe Leu Lys Ala Phe Ser Glu
 165 170 175
 Ala Glu Gln Thr Lys Leu Ala Met Leu Ser Gly Ile Leu Leu Gly Asn
 180 185 190
 Gly Thr Leu Pro Ala Thr Ile Leu Thr Ser Leu Phe Thr Asp Ser Leu
 195 200 205
 Val Lys Glu Gly Ile Ala Ala Ser Phe Ala Val Lys Leu Phe Lys Ala
 210 215 220
 Trp Met Ala Glu Lys Asp Ala Asn Ser Val Thr Ser Ser Leu Arg Lys
 225 230 235 240
 Ala Asn Leu Asp Lys Arg Leu Leu Glu Leu Phe Pro Val Asn Arg Gln
 245 250 255
 Ser Val Asp His Phe Ala Lys Tyr Phe Thr Asp Ala Gly Leu Lys Glu
 260 265 270
 Leu Ser Asp Phe Leu Arg Val Gln Gln Ser Leu Gly Thr Arg Lys Glu
 275 280 285
 Leu Gln Lys Glu Leu Gln Glu Arg Leu Ser Gln Glu Cys Pro Ile Lys
 290 295 300
 Glu Val Val Leu Tyr Val Lys Glu Glu Met Lys Arg Asn Asp Leu Pro
 305 310 315 320
 Glu Thr Ala Val Ile Gly Leu Leu Trp Thr Cys Val Met Asn Ala Val
 325 330 335
 Glu Trp Asn Lys Lys Glu Glu Leu Val Ala Glu Gln Ala Leu Lys His
 340 345 350
 Leu Lys Gln Tyr Ala Pro Leu Leu Ala Val Phe Ser Ser Gln Gly Gln
 355 360 365
 Ser Glu Leu Val Leu Leu Gln Lys Val Gln Glu Tyr Cys Tyr Asp Asn
 370 375 380
 Ile His Phe Met Lys Ala Phe Gln Lys Ile Val Val Leu Phe Tyr Lys
 385 390 395 400
 Ala Asp Val Leu Ser Glu Glu Ala Ile Leu Lys Trp Tyr Lys Glu Ala
 405 410 415
 His Ala Ala Lys Gly Lys Ser Val Phe Leu Asp Gln Met Lys Lys Phe
 420 425 430
 Val Glu Trp Leu Gln Asn Ala Glu Glu Glu Ser Glu Ser Glu Gly Glu
 435 440 445
 Glu Ser
 450

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1463 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HW094

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 255..1238

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1050..1355
 (D) OTHER INFORMATION: /label= SAC_23896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GTGACCCCCG AACACCCACA CTCGGTCCCC AGCCGTTTT CTCCCAGAGA TCCGGAAGCC	60
CCGACGTCGT GCCCTACACC AAAGATCGAG AAAACCACTC AGACGCGGCT CCTAGGCCGC	120
AGTCGGTTTC CCATAGCAAC CCTCGGAGCA CCCGCATCCC GCTTCCGGCC GGGTGGCTCG	180
GGCGCTCCCG TGACGTCACCG GCGCCGCTTT CGGGTGACTG AGTCGAGCTG AGGTTGTTGT	240
GGGCCGGGGGG CGCC ATG GGG GCG ACT GGC GAC ACC GAG CAG CCG CGG GGC Met Gly Ala Thr Gly Asp Thr Glu Gln Pro Arg Gly	290
1 5 10	
CCC GGC GGG GCG GAG CGA GGC GGC CTG GAG CTG GGC GAC GCG GGC GCG Pro Gly Gly Ala Glu Arg Gly Gly Leu Glu Leu Gly Asp Ala Gly Ala	338
15 20 25	
GCG GGC CAG CCG GTT CTC ACG AAC CCT TGG AAC ATA ATG ATC AAA CAC Ala Gly Gln Pro Val Leu Thr Asn Pro Trp Asn Ile Met Ile Lys His	386
30 35 40	
CGG CAG GTG CAG CGA AGA GGC CGC CGA TCT CAG ATG ACC ACA AGT TTC Arg Gln Val Gln Arg Arg Gly Arg Arg Ser Gln Met Thr Thr Ser Phe	434
45 50 55 60	
ACA GAT CCA GCC ATC TCT ATG GAT CTC CTC CGT GCT GTC CTG CAG CCT Thr Asp Pro Ala Ile Ser Met Asp Leu Leu Arg Ala Val Leu Gln Pro	482
65 70 75	
AGC ATC AAT GAG GAG ATC CAG AGT GTC TTC AAC AAG TAC ATG AAG TTC Ser Ile Asn Glu Glu Ile Gln Ser Val Phe Asn Lys Tyr Met Lys Phe	530
80 85 90	
TTC CAG AAG GCA GCG CTG AAT GTG CGA GAC AAC GTT GGT GAA GAG GTG Phe Gln Lys Ala Ala Leu Asn Val Arg Asp Asn Val Gly Glu Glu Val	578
95 100 105	
GAT GCA GAA CAG TTG ATT CAG GAG GCC TGC CGC AGC TGC CTG GAG CAG Asp Ala Glu Gln Leu Ile Gln Glu Ala Cys Arg Ser Cys Leu Glu Gln	626
110 115 120	

GCA AAG CTA CTC TTT TCA GAT GGA GAA AAA GTG ATA CCC AGA TTG GCC Ala Lys Leu Leu Phe Ser Asp Gly Glu Lys Val Ile Pro Arg Leu Ala 125 130 135 140	674
CAT GAA CTT CCA GGG ATC AAG CGT GGC CGG CAG GCA GAA GAG GAG TCC His Glu Leu Pro Gly Ile Lys Arg Gly Arg Gln Ala Glu Glu Ser 145 150 155	722
CAC CGA GGA AGC CCC ATT CCC AAA AAG AGG AAA GGT CGG CCT CCT GGA His Arg Gly Ser Pro Ile Pro Lys Lys Arg Lys Gly Arg Pro Pro Gly 160 165 170	770
CAT GTC CTG TCA AAT GAC CGC GCA GCT GCT GGC ATG GTA TGG AAA CCA His Val Leu Ser Asn Asp Arg Ala Ala Gly Met Val Trp Lys Pro 175 180 185	818
AAA TCC TGT GAA CCA ATT CGC CGA GAA GGC CCC AAG TGG GAC CCA GCT Lys Ser Cys Glu Pro Ile Arg Arg Glu Gly Pro Lys Trp Asp Pro Ala 190 195 200	866
CGG CTG AAT GAA TCT ACC ACC TTT GTT TTG GGG TCT CGA GCC AAC AAG Arg Leu Asn Glu Ser Thr Thr Phe Val Leu Gly Ser Arg Ala Asn Lys 205 210 215 220	914
GCC TTA GGG ATG GGA GGC ACC AGA GGG AGG ATT TAC ATC AAG CAC CCA Ala Leu Gly Met Gly Gly Thr Arg Gly Arg Ile Tyr Ile Lys His Pro 225 230 235	962
CAC CTC TTT AAG TAT GCA GCA GAT CCT CAG GAC AAG CAC TGG CTG GCT His Leu Phe Lys Tyr Ala Ala Asp Pro Gln Asp Lys His Trp Leu Ala 240 245 250	1010
GAG CAG CAT CAT ATG CGG GCA ACA GGA GGA AAG ATG GCG TAC CTT CTC Glu Gln His His Met Arg Ala Thr Gly Gly Lys Met Ala Tyr Leu Leu 255 260 265	1058
ATT GAG GAA GAC ATC CGA GAC TTG GCT GCC AGC GAT GAC TAC AGA GGA Ile Glu Glu Asp Ile Arg Asp Leu Ala Ala Ser Asp Asp Tyr Arg Gly 270 275 280	1106
TGC TTG GAC CTG AAG TTG GAG CTG AAG TCC TTT GTT TTG CCA TCC Cys Leu Asp Leu Lys Leu Glu Leu Lys Ser Phe Val Leu Pro Ser 285 290 295 300	1154
TGG ATG GTT GAG AAG ATG CGG AAA TAC ATG GAG ACA CTA CGG ACA GAA Trp Met Val Glu Lys Met Arg Lys Tyr Met Glu Thr Leu Arg Thr Glu 305 310 315	1202
AAT GAG CAT CGT GCT GCT GAA GCA ACT CCC CAG ACC TGAGCCGAGT Asn Glu His Arg Ala Ala Glu Ala Thr Pro Gln Thr 320 325	1248
GTCCCTGGCTA CTACACTTGG CAGTCTGCCT CCCAGACCT CTTTCCCCGC CCGGCTGAGG	1308
CCATCATGGG GATGCGGTCT AGTTGGCTCT TAGCAGCATC AAGCTGTACA TGAGCTAGTT	1368
TGTAGTGACT CACTGCAGAG CCCCCCAGAC TGGCTTGTGG TTCTGTTCT AAAGTTATTG	1428
GAATAAGAAG CAATTAAACA AGTTTGTAAT AAAAAA	1463

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met Gly Ala Thr Gly Asp Thr Glu Gln Pro Arg Gly Pro Gly Gly Ala
 1 5 10 15

Glu Arg Gly Gly Leu Glu Leu Gly Asp Ala Gly Ala Ala Gly Gln Pro
 20 25 30

Val Leu Thr Asn Pro Trp Asn Ile Met Ile Lys His Arg Gln Val Gln
 35 40 45

Arg Arg Gly Arg Arg Ser Gln Met Thr Thr Ser Phe Thr Asp Pro Ala
 50 55 60

Ile Ser Met Asp Leu Leu Arg Ala Val Leu Gln Pro Ser Ile Asn Glu
 65 70 75 80

Glu Ile Gln Ser Val Phe Asn Lys Tyr Met Lys Phe Phe Gln Lys Ala
 85 90 95

Ala Leu Asn Val Arg Asp Asn Val Gly Glu Glu Val Asp Ala Glu Gln
 100 105 110

Leu Ile Gln Glu Ala Cys Arg Ser Cys Leu Glu Gln Ala Lys Leu Leu
 115 120 125

Phe Ser Asp Gly Glu Lys Val Ile Pro Arg Leu Ala His Glu Leu Pro
 130 135 140

Gly Ile Lys Arg Gly Arg Gln Ala Glu Glu Ser His Arg Gly Ser
 145 150 155 160

Pro Ile Pro Lys Lys Arg Lys Gly Arg Pro Pro Gly His Val Leu Ser
 165 170 175

Asn Asp Arg Ala Ala Ala Gly Met Val Trp Lys Pro Lys Ser Cys Glu
 180 185 190

Pro Ile Arg Arg Glu Gly Pro Lys Trp Asp Pro Ala Arg Leu Asn Glu
 195 200 205

Ser Thr Thr Phe Val Leu Gly Ser Arg Ala Asn Lys Ala Leu Gly Met
 210 215 220

Gly Gly Thr Arg Gly Arg Ile Tyr Ile Lys His Pro His Leu Phe Lys
 225 230 235 240

Tyr Ala Ala Asp Pro Gln Asp Lys His Trp Leu Ala Glu Gln His His
 245 250 255

Met Arg Ala Thr Gly Gly Lys Met Ala Tyr Leu Leu Ile Glu Glu Asp
 260 265 270

Ile Arg Asp Leu Ala Ala Ser Asp Asp Tyr Arg Gly Cys Leu Asp Leu
 275 280 285

Lys Met Arg Lys Tyr Met Glu Thr Leu Arg Thr Glu Asn Glu His Arg
305 310 315 320

Ala Ala Glu Ala Thr Pro Gln Thr
325

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 1276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HW095

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 7..876

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: complement (631..798)

(D) OTHER INFORMATION: /label= SAC_23802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTCGAC ATT TTC TCA GAA TCC TAC GGA GGA AAG ATG GCT GCT GGC ATC 48
 Ile Phe Ser Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile
 1 5 10

AGT TTA GAA CTT CAC AAG GCT ATT CAG CAA GGG ACC ATC AAG TGC AAC
 Ser Leu Glu Leu His Lys Ala Ile Gln Gln Gly Thr Ile Lys Cys Asn
 15 20 25 30

TTC TCT GGG GTT GCT TTG GGT GAC TCC TGG ATC TCC CCT GTG GAT TCA
 Phe Ser Gly Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser
 35 40 45

GTG CTG TCC TGG GGA CCT TAC CTG TAC AGC GTG TCT CTC CTT GAT AAT
 Val Leu Ser Trp Gly Pro Tyr Leu Tyr Ser Val Ser Leu Leu Asp Asn
 50 55 60

AAA GGC TTG GCT GAG GTG TCC GAC ATT GCG GAG CAA GTC CTC AAT GCT 240
 Lys Gly Leu Ala Glu Val Ser Asp Ile Ala Glu Gln Val Leu Asn Ala
 65 70 75

GTA AAC AAG GGC TTC TAC AAG GAA GCC ACT CAG CTG TGG GGG AAA GCA 288
 Val Asn Lys Gly Phe Tyr Lys Glu Ala Thr Gln Leu Trp Gly Lys Ala
 80 85 90

GAA ATG ATC ATT GAA AAG AAC ACC GAC GGG GTA AAC TTC TAT AAC AAC ATC
 Glu Met Ile Ile Glu Lys Asn Thr Asp Gly Val Asn Phe Tyr Asn Ile 336

95	100	105	110	
TTA ACT AAA AGC ACC CCC GAC ACC TCT ATG GAG TCG AGC CTC GAG TTC Leu Thr Lys Ser Thr Pro Asp Thr Ser Met Glu Ser Ser Leu Glu Phe 115 120 125				384
TTC CGG AGC CCC TTA GTT CGT CTC TGT CAG CGC CAC GTG AGA CAC CTA Phe Arg Ser Pro Leu Val Arg Leu Cys Gln Arg His Val Arg His Leu 130 135 140				432
CAA GGA GAC GCC TTA AGT CAG CTC ATG AAC GGT CCC ATC AAA AAG AAG Gln Gly Asp Ala Leu Ser Gln Leu Met Asn Gly Pro Ile Lys Lys Lys 145 150 155				480
CTC AAA ATT ATC CCT GAC GAT GTC TCC TGG GGA GCC CAG TCA TCC TCC Leu Lys Ile Ile Pro Asp Asp Val Ser Trp Gly Ala Gln Ser Ser Ser 160 165 170				528
GTC TTC ATA AGC ATG GAA GAG GAC TTC ATG AAG CCT GTC ATC GAC ATC Val Phe Ile Ser Met Glu Glu Asp Phe Met Lys Pro Val Ile Asp Ile 175 180 185 190				576
GTG GAT ACG TTG CTG GAA CTC GGG GTC AAT GTG ACT GTG TAC AAT GGG Val Asp Thr Leu Leu Glu Leu Gly Val Asn Val Thr Val Tyr Asn Gly 195 200 205				624
CAG CTG GAT CTC ATT GTG GAC ACC ATA GGT CAG GAG TCC TGG GTT CAG Gln Leu Asp Leu Ile Val Asp Thr Ile Gly Gln Glu Ser Trp Val Gln 210 215 220				672
AAG CTG AAG TGG CCA CAG CTG TCC AGA TTC AAT CAG CTA AAA TGG AAG Lys Leu Lys Trp Pro Gln Leu Ser Arg Phe Asn Gln Leu Lys Trp Lys 225 230 235				720
GCC CTG TAC ACC AAT CCT AAG TCT TCA GAA ACA TCT GCG TTT GTC AAG Ala Leu Tyr Thr Asn Pro Lys Ser Ser Glu Thr Ser Ala Phe Val Lys 240 245 250				768
TCC TAT GAG AAC CTA GCG TTC TAC TGG ATC CTA AAG GCG GGT CAC ATG Ser Tyr Glu Asn Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met 255 260 265 270				816
GTT CCT GCT GAC CAA GGG GAC ATG GCT CTG AAG ATG ATG AGG CTG GTT Val Pro Ala Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val 275 280 285				864
ACT CAG CAG GAG TAGCTGAGCT GAGCTGGCCC TGGAGGCCCT GGAGGCCCTG Thr Gln Gln Glu 290				916
GAGGCCCTGG AGTAGGGCCC AGGATGCAGG TGCTAATGTC TATCCCCGGC GCTCTTCTTC				976
CCGACTCTAC CATGGGATGT AACTCCAGGA GCCCCTGCCA TCTCCGGTAC CAAAAGACTG				1036
TGGCTTCCGT GTCTACTCAG AAATCAGTTC TACTTCGTAACAGTGTAA AAACCAGACT				1096
CATTTAACCA GAGTGAAGGA TTGCACTCCA TTGGCTTCTT AGCACAGAAG CAGCTGATAA				1156
CACAAAGTAAA CCCAGGCCCT TGAGAGGTAG AAGCAAGAGG ATCAGAGGTT CAAGCGCATC				1216
CTCGGCTCCA TCACAAGTTC AAAAGCCGCC TGCACCAAAT GGGAGTCCTT GTCTAAAAAA				1276

WO 98/53071

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Ile Phe Ser Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Ser Leu
 1 5 10 15

Glu Leu His Lys Ala Ile Gln Gln Gly Thr Ile Lys Cys Asn Phe Ser
 20 25 30

Gly Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu
 35 40 45

Ser Trp Gly Pro Tyr Leu Tyr Ser Val Ser Leu Leu Asp Asn Lys Gly
 50 55 60

Leu Ala Glu Val Ser Asp Ile Ala Glu Gln Val Leu Asn Ala Val Asn
 65 70 75 80

Lys Gly Phe Tyr Lys Glu Ala Thr Gln Leu Trp Gly Lys Ala Glu Met
 85 90 95

Ile Ile Glu Lys Asn Thr Asp Gly Val Asn Phe Tyr Asn Ile Leu Thr
 100 105 110

Lys Ser Thr Pro Asp Thr Ser Met Glu Ser Ser Leu Glu Phe Phe Arg
 115 120 125

Ser Pro Leu Val Arg Leu Cys Gln Arg His Val Arg His Leu Gln Gly
 130 135 140

Asp Ala Leu Ser Gln Leu Met Asn Gly Pro Ile Lys Lys Lys Leu Lys
 145 150 155 160

Ile Ile Pro Asp Asp Val Ser Trp Gly Ala Gln Ser Ser Val Phe
 165 170 175

Ile Ser Met Glu Glu Asp Phe Met Lys Pro Val Ile Asp Ile Val Asp
 180 185 190

Thr Leu Leu Glu Leu Gly Val Asn Val Thr Val Tyr Asn Gly Gln Leu
 195 200 205

Asp Leu Ile Val Asp Thr Ile Gly Gln Glu Ser Trp Val Gln Lys Leu
 210 215 220

Lys Trp Pro Gln Leu Ser Arg Phe Asn Gln Leu Lys Trp Lys Ala Leu
 225 230 235 240

Tyr Thr Asn Pro Lys Ser Ser Glu Thr Ser Ala Phe Val Lys Ser Tyr
 245 250 255

Glu Asn Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val Pro
 260 265 270

Ala Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val Thr Gln
275 280 285

Gln Glu
290

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2421 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - vii) IMMEDIATE SOURCE:
 - (B) CLONE: HW096
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 295..1302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTCGACGTCT GATTTTACAT TCATGCAGTT GGGAGTAAGA GGAAAAAGAT TCTGAAGTGT	60
GGGGAACCTTC ACAAAAGAGGG GAACAAAGTC TGTGTCTATG GCTCCAAGGG AGAGAACATC	120
AGAGACACTC TGAGGAAGGA CGGCAGGTTTG TGTCTTTCA TAGAGAATAA CCATTGGAAA	180
CTCATTAATG ACCTGGACAC TATCATAGAA AACACTCAGC CATTGATGA GTTGGAGGGC	240
AAGCTCTTTC AGGTTGCAGC TGAGCTACCA AAGAACCCCTA GGGTAGTCTC TGTC ATG	297
Met 1	
CAG AAT TCT GGG TTA GAG AAC AGA GAC TTC CAT AAG CTA GAA GAC TAT	345
Gln Asn Ser Gly Leu Glu Asn Arg Asp Phe His Lys Leu Glu Asp Tyr	
5 10 15	
ATT GTG AAT GCG AAC CCT ACA TTG AAA GAA GAA GGA GAA AAA CTC AGA	393
Ile Val Asn Ala Asn Pro Thr Leu Lys Glu Glu Gly Glu Lys Leu Arg	
20 25 30	
GCA TAC ATC AAG AAA GAA AGT AAA AAA AGA AAG AAA GGT TCC TTA TTC	441
Ala Tyr Ile Lys Lys Glu Ser Lys Lys Arg Lys Lys Gly Ser Leu Phe	
35 40 45	
AAA GTG CAT AAA GAA CAC TTT GGG AAA ATA ACA AAA AAT TCT ACT CCT	489
Lys Val His Lys Glu His Phe Gly Lys Ile Thr Lys Asn Ser Thr Pro	
50 55 60 65	
GTT AAA GTG CAC AAA CAT CTT TCG AAA GTC AGT GAT TCA GTT GGG TTC	537
Val Lys Val His His Leu Ser Lys Val Ser Asp Ser Val Gly Phe	
70 75 80	
CTA TGG TGG AAC AAC AAT GGA AAG GAG GGC TGT GCC ACC TGC TTT GTT	585
Leu Trp Trp Asn Asn Asn Gly Lys Glu Gly Cys Ala Thr Cys Phe Val	

85	90	95	
TTT AAA GGA TTA TAC ATT TTG ACT TGC CGG CAT GTG ATA ACT AGT ATT Phe Lys Gly Leu Tyr Ile Leu Thr Cys Arg His Val Ile Thr Ser Ile 100	105	110	633
GTG GGT GAA GGC ATA GAT CCA TGT CAG TGG GCA AGC TTA ATT AGT CAG Val Gly Glu Gly Ile Asp Pro Cys Gln Trp Ala Ser Leu Ile Ser Gln 115	120	125	681
TGT GTA AAG GTG ACC TTT GGT TAT GAA GAG TTC CCA CTA GTA GAA GAC Cys Val Lys Val Thr Phe Gly Tyr Glu Glu Phe Pro Leu Val Glu Asp 130	135	140	729
AAG TTT TTT GAG GTT AAA CCT TGG TTT GAG ATA TCT AAT GAA AGC CTT Lys Phe Phe Glu Val Lys Pro Trp Phe Glu Ile Ser Asn Glu Ser Leu 150	155	160	777
GAC TAT GCT GTC CTA GAA CTG AGG GAA AAT GGA CAA GAA GTT CCT GCT Asp Tyr Ala Val Leu Glu Leu Arg Glu Asn Gly Gln Glu Val Pro Ala 165	170	175	825
GGA CTG TAT AAT GGA ATA GGA CCT GTG CCA CTT GGT GGG TTA ATA TAT Gly Leu Tyr Asn Gly Ile Gly Pro Val Pro Leu Gly Leu Ile Tyr 180	185	190	873
ATC ATT GGC CAT CCT GAT GGA GAA AAG AAG TCT ACT GAT GGC TGT GCA Ile Ile Gly His Pro Asp Gly Glu Lys Lys Ser Thr Asp Gly Cys Ala 195	200	205	921
GTG GTC CCT CAA AGT CAT AGA GGG CAA AAA TGT CAG GAA AAT TTT CAA Val Val Pro Gln Ser His Arg Gly Gln Lys Cys Gln Glu Asn Phe Gln 210	215	220	969
GCA AGA GAG AAA GCA AAC TAC TGG ATT TCT ACA TCT TTT TTT CCT ATA Ala Arg Glu Lys Ala Asn Tyr Trp Ile Ser Thr Ser Phe Phe Pro Ile 230	235	240	1017
TAC ACA CAA AGA AGT TTC CAC GAA GTC TTT CAC AAC CAT GAT GTG GTT Tyr Thr Gln Arg Ser Phe His Glu Val Phe His Asn His Asp Val Val 245	250	255	1065
ACT TAT GAC ACC ACT TTT TTT GGT GGG TCT TCT GGA TCC CCA GTA TTT Thr Tyr Asp Thr Thr Phe Phe Gly Gly Ser Ser Gly Ser Pro Val Phe 260	265	270	1113
GAT TCT AAT GGT TCA TTG GTG GCC ATG CAT GCT GCT GGC ATC ACT TGT Asp Ser Asn Gly Ser Leu Val Ala Met His Ala Ala Gly Ile Thr Cys 275	280	285	1161
ACA GAC CAG AAT GGA GTT TTT AAT ATC ATT GAG TTT GGT TTT ACT ATG Thr Asp Gln Asn Gly Val Phe Asn Ile Ile Glu Phe Gly Phe Thr Met 290	295	300	1209
GAA TCC ATT CTT GCT AAT ATT AAG CAA ACT AAA GAG TGG TAT GAT ACC Glu Ser Ile Leu Ala Asn Ile Lys Gln Thr Lys Glu Trp Tyr Asp Thr 310	315	320	1257
ATT TTT GTA AAT GAT CGG GAT GCA GAA ATG CTG AGC ACA GAC TCC Ile Phe Val Asn Asp Arg Asp Ala Glu Met Leu Ser Thr Asp Ser 325	330	335	1302
TGAGGACTGG AAAGGGTGTA TTCTAGTTCA CAACTTTAAG GGAATTGCCT AAGGTGTTTT			1362

TCTTCAGATA ATAATGTTT ATGAACCTTC AAAATGATTA ATTTCACCCA ATAATCATAG	1422
TTCTAGAGTG TATCTTAACT ATCAAGCATT TTCATGGTT ATTAAAACAA ACAATCAAA	1482
ACAAAACAT CAGTTGAAC TTTGTGAA AGTAGCATGA AAAAGAGGAT TAAGTGCTGA	1542
TGTGGGATCC GAGGGTCAGG AGATGCTAAG ATGTAAAAA GTTGGAGAGCA TAAACTGGAG	1602
TTATTAGCCA GAAGATTCAAT GGAAAAGAAA GAAGCCTACC ACGTTCCCTTG AAACCTTAAAC	1662
CAATTTCAAA CTCACTCATT TGGTTCTACC CATATCTTCC TTCTCTGCTG ACCAGAGCTC	1722
AGCCAGGACA CTGAATCACA GCGACTTAAC CCTCCCAGGG CCCTGAACAT GGTGGCATTT	1782
CTTCCATTAA GTCTTTTAA CTTAACAGACT AGATCTGAAA TGAACCCACA TGAAGTGGCA	1842
TGGAAATCAT TGAGCAAGCA AGGAGCTGGT CTCTGCCACA GAATGCATGT ACCTGAGACT	1902
TTCTGGACTT GAGTTGTGGA GAGCAAACAT TGGAATAGGT GGTTTCTACT TGATACGATT	1962
CACAATGGAG AGTGCTAGGA GGATATTGGG CACAACCTAG GACAATTCTC AGCAGTGTGA	2022
CACTCAAGTC TTGGTCCTT GAAGAGAAAG AAAACTGCGT TCAAGAAGTA ATCTCATCAA	2082
AAACAGAGTC AAGGAGAAATT TATGAACAGA AGACCAGAGA TCTTAGATTA TTTGAGAGAA	2142
AGTAGGAATA GATGAGATGC TGAAGGAATG TTGCTGGGAT CCAGCGATTG CTTCAATTCT	2202
TCCTTTATCA TAACTGAAAT ATGTCCTGTA TGAGAGCTAA CATGATCCTA ATCCACAACT	2262
CCCCCTTATTT TCCAGACATT TCCTAGTGCT ATTGTGTGAT ATTTGTGTC CCCTGCCAA	2322
TGTATTTTTC CCAAATCAA TACAGGTGAA TCAATTAAA AACAGTGTAA TATCTGTAGT	2382
AGGTTTGAA ATATAAGATG AAAAATTAA AAAGTCGAC	2421

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Met	Gln	Asn	Ser	Gly	Leu	Glu	Asn	Arg	Asp	Phe	His	Lys	Leu	Glu	Asp
1				5				10				15			
Tyr	Ile	Val	Asn	Ala	Asn	Pro	Thr	Leu	Lys	Glu	Glu	Gly	Glu	Lys	Leu
								20		25			30		
Arg	Ala	Tyr	Ile	Lys	Lys	Glu	Ser	Lys	Lys	Arg	Lys	Lys	Gly	Ser	Leu
				35				40				45			
Phe	Lys	Val	His	Lys	Glu	His	Phe	Gly	Lys	Ile	Thr	Lys	Asn	Ser	Thr
				50				55				60			
Pro	Val	Lys	Val	His	Lys	His	Leu	Ser	Lys	Val	Ser	Asp	Ser	Val	Gly
				65				70				75			80

Phe	Leu	Trp	Trp	Asn	Asn	Gly	Lys	Glu	Gly	Cys	Ala	Thr	Cys	Phe	
				85				90						95	
Val	Phe	Lys	Gly	Leu	Tyr	Ile	Leu	Thr	Cys	Arg	His	Val	Ile	Thr	Ser
				100				105					110		
Ile	Val	Gly	Glu	Gly	Ile	Asp	Pro	Cys	Gln	Trp	Ala	Ser	Leu	Ile	Ser
				115				120				125			
Gln	Cys	Val	Lys	Val	Thr	Phe	Gly	Tyr	Glu	Glu	Phe	Pro	Leu	Val	Glu
				130				135				140			
Asp	Lys	Phe	Phe	Glu	Val	Lys	Pro	Trp	Phe	Glu	Ile	Ser	Asn	Glu	Ser
				145				150			155			160	
Leu	Asp	Tyr	Ala	Val	Leu	Glu	Leu	Arg	Glu	Asn	Gly	Gln	Glu	Val	Pro
				165				170					175		
Ala	Gly	Leu	Tyr	Asn	Gly	Ile	Gly	Pro	Val	Pro	Leu	Gly	Gly	Leu	Ile
				180				185				190			
Tyr	Ile	Ile	Gly	His	Pro	Asp	Gly	Glu	Lys	Lys	Ser	Thr	Asp	Gly	Cys
				195				200				205			
Ala	Val	Val	Pro	Gln	Ser	His	Arg	Gly	Gln	Lys	Cys	Gln	Glu	Asn	Phe
				210				215			220				
Gln	Ala	Arg	Glu	Lys	Ala	Asn	Tyr	Trp	Ile	Ser	Thr	Ser	Phe	Phe	Pro
				225				230			235			240	
Ile	Tyr	Thr	Gln	Arg	Ser	Phe	His	Glu	Val	Phe	His	Asn	His	Asp	Val
				245				250				255			
Val	Thr	Tyr	Asp	Thr	Thr	Phe	Phe	Gly	Gly	Ser	Ser	Gly	Ser	Pro	Val
				260				265			270				
Phe	Asp	Ser	Asn	Gly	Ser	Leu	Val	Ala	Met	His	Ala	Ala	Gly	Ile	Thr
				275				280			285				
Cys	Thr	Asp	Gln	Asn	Gly	Val	Phe	Asn	Ile	Ile	Glu	Phe	Gly	Phe	Thr
				290				295			300				
Met	Glu	Ser	Ile	Leu	Ala	Asn	Ile	Lys	Gln	Thr	Lys	Glu	Trp	Tyr	Asp
				305				310			315			320	
Thr	Ile	Phe	Val	Asn	Asp	Arg	Asp	Ala	Glu	Met	Leu	Ser	Thr	Asp	Ser
				325				330				335			

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 836 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HW097

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: complement (203..553)
 (D) OTHER INFORMATION: /label= SAC_23978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GTCGACTATT ACTATAGCCT TGTATATACT CCCCTCCGGC CCTGTTTGTC TCAGTCCCAC	60
TCCCTCTTGT CTCTGAGAAT CATCCCCAG CCCCAAGTTC TCCCTTCTGT CTCCCCCAC	120
CCCCCCTGCC TCCCATTCTC CTGTCTCTGA ATGCCTTGC CTGTATAAAAG AGTTGGATT	180
TCCCCCTGGTG TCTGTACTGT GTACACACAT CCCTTGAGA AGCACAAGGA GATGACACGC	240
GCATTGTAAC CTTCACACTG TCTCGGTGGC GACATAAAAGG AAGCTGTGAA TTACAAGCTC	300
TGCCCTTTTC TGGCCTCTCC CTCGGCCCCC ATGACCGGGGG CACTCTCTGC CCTCCCCACG	360
GCCTTAACAT GTTCCTGCTC CACCTATCCT GGTGCCCTT GTCTGGCTGA CTGTAGCCTC	420
CCTGAGGGAA GGGATTGCTG GAGAGGTAGC TCCTATCCAG GAATGAAGGA CACTGGCTGG	480
AAACTAAGCC AAGAATGTTA CAGACAGGGG GAGCTGGGA TTGGTGACTG ACCCTTGCAG	540
TTGGGCAGTG AGTACCCAAG GCCAGAACCT GAAGCCCTCA TTCATTCACTG GGCCTTTCTT	600
TCCTCAGGGT GCCCAGTGCC CTGTCCCTCAC TTTGATGCC AGGCCCACTG CTTGCATTTT	660
CTGGTGAGCC AGGGCTTGGT CATGTGAGGA AAGAGGTAGG CCTAGAGCAG GAGTTGAAAG	720
CCCTGCTGTT GTGTGTCCCT ACCATACAGG GCTGGCTAAA AGTCGAGGTA GACGCTTATC	780
TAGGAAGCGC AAGGCCCTGG GTTCGGTCCC CAGCTCGGAA AAAAAGAAC CAAAAAA	836

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: SAC23798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GGGGGATCCG CCCGATCCAA GACTGCCAG GGTGGCTGCT CCATCTCACC CAGAGCAACC	60
--	----

GGAGCTGGAC CTGGGGGTCG GAGCACTTCG AAGGTGATGG GTTATGGTGC CGCCTGCTGG	120
ACATAGTTGT CCAGAGCTCT TCCTGAAAGG TTTGCTACAG GATTGCCCT TCTCATCCAG	180
TCTAAGAAAC TACTTAGTCA ACTCCTAGTG TCTAAGCAGA AGGCTTCAGC TATGGCTTCT	240
CCCCTGGGG AGGAAGAGGA AGAGGTACAA ATTCTTGTCT TGCTGCTCCC AGGGAAAAGA	300
TCGGGCTAGA GCGGCCGC	318

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: SAC_23800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GGGGGATCCG CCCGATCACA CGGCTGCCCT CTGGTATACA GCAGAGGGGA ATGCCAAGGT	60
ATAAGTATCC TTCAATTCCCT TCTTGCAC ATACCAGCAT TTCTTGCCTT TTTTGGCATT	120
CTACCTCTTC TTTGACAGCA CTGAGACTGT TAAGTGCTGC ATACAAGCTA CTTGTCTCCC	180
TATCTGTNNG CACATGTTTC ATGTCATGAA GATGATAAGG TCAGGCAAAG AGGCATGAAG	240
ATTCCTGAAT AGTGCCCCAGA TCGGGCTAGA GCGGCCGC	278

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 393 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: SAC_23801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GGGGGATCCG CCCGATCCAG TAGCGACAGC CCTGGCCCT GACGAGGATG GAAGTGACGT	60
TGTAGCNATT GTCTTCCTGT AGCTCATAGA TGGTGCTGTN NATGGTAAAG CGGCTTTGTC	120

TTTCTTCCTG GACCGCATTG CCTGCCAGGN NGACAACGAA CCACCTGCC CGGAACCGTT	180
CGGTCCAGAA GCCTGGCTGC AGGGGCACAC TGATCGATCC AGTAGCGACA GCCCTGGCCC	240
CTGACCGAGGA TGGAAAGTGAC GTTGTAGCTA TTGCTTCCT GTAGCTCAT AATGGTGCTG	300
TACATGGTAA AGCGGCTTTG TCTTTCTTTC TGGACCGCAT TGCCTGCCAG GCCGACAACG	360
AACCACCTGC CCTGGAACCG TTCGGTCCAG AAG	393

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: SAC_23833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GGGGGATCCG CCCGATCTGT ATCTCGTCCC TTGGCTGGCT GAGCCTCTGG AGGAGGTGTC	60
CAAAGCCCCG GTGGATTCT GTCTCAGGGG TCTCTGTGAG ATTGAACCTTG AGACCTTCTA	120
GAATCTCTTC CATGCTGTTG CCCTTTGCTC CCAGGGACAC GACGGCCAAG GCGGCTGAGA	180
TGCTAAGTGG GGAGAAGACA ACATTTTAT CTGGATTCT CAAAGCCAGC TTCTGTAGA	240
GGCTGAAGGC AAAGTCAGTA TTGATGGAAG CCAGTGTGAG ACTGTCCAGT TGTGTCCCCCT	300
TGTCTGGTC TTCATGGAAT AGAGTGTCT CTCCCACTAT GCAAATCTGG GAAGCAGAGG	360
AGAGCAGAGC CCGATCGATC AAGATGACTA AGATGCTCAA AGGATTGAC GCTGTGGAA	420
ATGCCACAGG TTCCGGTTC GCCTACACCC CAGCTATGGA GAGCCTCTGT GGATATGTCA	480
CAAGTCCAGA ACCGCAGCGA GGAGTTCTC ATCGGGGCC GTTTAAGGAC G	531

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: SAC_23836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GGGGGATCCG CCCGATCATG ATGAATCCCC TGGGACCAAG CTATAACACA CAGTCCTCTG	60
AGAAAAAAGGA TTGTGGTTTG CAGCAAATTTC AGCCAATTTC GTCAAGCAAT TTGTGAGAGA	120
CACTCCTTAC TTGGTTGTTT CCTTCTCAGT CTTACGGGGT GCCTTATCAC TCCGTGATGG	180
TTCATGGCCA CACAGTCATA TTTCAGGGAG AAGTCCTTGT CGGTCACACC AGTTATCCTT	240
AACAGTGAGG TTAAGCAAAT CATGCCATTG CTGG	274

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: SAC_23853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GGGGGATCCG CCCGATCGTG TTATTGAGGT CATCCACGGT GGAGATTAGC AGGTGACTCC	60
GTTTTCCTGG AAATGAGTGG AGTTGGGAAG GGGACCCGTG GCCGTGCTCC AGCTATAGTT	120
GGTGGGCGGT GGTTCGCTGC GAGCTTCACA GGTCAAGGTT ACAGTTAGTAG GCCCAATGTA	180
CCAGTTGCCT TCATAGCCAG AGATGGACAC TTCCGGTGGA TAAGGTAGGG AAAGGATCGG	240
GCTAGAGCGG CCGC	254

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 255 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: SAC_23906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GGGGGATCCG CCCACAGAAC CCAGAGGAAG GAGAGGCTGC TGGGGTGGAG GCCTAGGC	60
TGGAGACATG TGGAGTTCTC TAGGGGTCTG CAGCAACCTC GGAAAGCTGG GAGATTCC	120
CCTTGAGACT CCTACATATA GAAAATGAT GCTTCTGTCT CATTCCATGC GGCTTC	180
GCGGTATTCC TGTAGCGCTT TCTCTGCCAC TGTGTCCATA AACTTAGGGT TATCCTTGG	240
GA CTTCTTCT GGTAC	255

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 219 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: SAC_23907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GGGGGATCCG CCCACCCCAT CTAATCCTCT GAGGCTCAGG GTGACTCATT CTTCTTGG	60
CCCAGGGGCG GGGCCGACAT TTGTTCCCCC AGTTGGGCC TGCTGCCCA GGCCAGTGG	120
ATTCCCACTG TCTCCAGCCA CTAAAGCCAC ATTCCCTCAGG TAGTTGGTAT TGAAGCAGTT	180
GGCTTGTGTTA TCTCCAGGAG ACAAGGTTCG AGCGGCCGC	219

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: SAC_23916

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GGGGGATCCG CCCTCGAGCG GCCGCCACA AGAGATTGAA CCTAGAGCTG TGTGCCTC	60
--	----

GGGCAAGCAC TCTCTACTGA GCTACATCCC TGTTAAAGTG CCTTTTTTGG GAGCTTGTC	120
TTCCAGCCTG CCAATCAACC CACTTTATGG GTGTGCCTAG ATTCCCCTTT CTCTGAGTAG	180
GG	182

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 191 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: SAC_23922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GGGGGATCCG CCCACTGTTC TCAAACAGTT GCCTAACAAAT ACATTTAATT AAGAAATTAT	60
CATAACTGTA TGCTTACACA TATGTGGATA GGCATCAATG AAGATTACAA CAGCTCAGCC	120
ACAGTGCTGC AATGCTCTAC ACTACTACAA AACACCCACC ACGGGCCTGN NACCTGCCCT	180
CGAGCGGCCG C	191

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: SAC_24030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GGGGGATCCG CCCACCATAT CTATACGGCC CTGGAAAGAGG AGATAGAGCG AAACAAGCAG	60
AACCCAGTCT ATGCCCGCT CTACTTNCT GAGGAGCTGC ACCGAAGGCT GCCCTAGAGC	120
AGGACATGGC CTTCTGGTAT GGGCCCCACT GGCAGGGAGGC CATCCCTTAN NNACCAGCCA	180
CACAGCACTA CGTAAAGCGT CTCCACGAGG TGGGAGGTGG GCTAGAGCGG CCGC	234

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 172 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: SAC_24078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGGGGATCCG CCCGATCAAG ATGACTAAGA TGCTCAAAGG ATTGACGCT GTGGAAATG	60
CCACAGGTTT CCGGTTGCC TACACCCCAG CCATGAGAGC CTCTGTGGAT ATGTCCACAA	120
GTCCCAGAAC CGCAGCGAG GAGTTTCTCA TCGCGGGCG TTTAAGGAAC GG	172

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: SAC_24105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GGGGGATCCG CCCGATCTGT GCATGTGAGC CGAACAGAAG TCAGCAATAA CCATGTCTTG	60
ATTTACCTGG ATAAGGTGTC AAATCAGACG GTGAACTTGT CCTTCACGGC TCAGCAAGAT	120
ATTCCAATAA GGGACCTGAA GCCAGCCGTA GTGAAAGTCT ACGATTACTA TGAGAAAGAT	180
GAGTTGCAG TTGAAAATA CAGCGCTCCC TGCAGCACAG ATTATGGAAA TGCCTGAGGA	240
C	241

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: SAC_24140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GGGGGATCCG CCCGATCCTT AAAGGTCCA TAACCAAGTA CTCCATGCAG TCATCTCCTC	60
TAACCTGTGG GTCCCCCTCCA TTCATTGCAA GCTGCTGGAC ATAGCCTGCT GGGTCCACCA	120
CAAGTACAAC AGTGACAAGT CCAGCACCTA TGTGAAGAAT GGACACATCCT TCGACATCCA	180
CTACGGCTCA GGTAGCCTCT CTGGGTACCT GAGCCAGGAC ACTGTGTTGG TTCC	234

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: SAC_24142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GGGGGATCCG CCCGATCTAT CGGGGTATAT TCGGAACGTGT GGAGTCTGAC CGCAGTGCAC	60
TGCTACTCACTCTGT CTCTTTCTCA CTGTGGGAGT AGCTATGGGA AAGGTCACAC	120
TTCCCTGCTT TCCCCTCAAA CCAACAGGGC TTTCACTTCT CAGTCTCCCA ACGCACTGCA	180
CACTGCTCCC AGCATCCCGC ACAGTCTCAC CACACAC	217

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: SAC_24192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GGGGGATCCG CCCACATCTC AGCGGTGGGG ACTCAGACAT TCCGTGTTT CCTCCTTGGC	60
CTCCAGCCTC TCTGTAGGAA CCTCCAGCAG CCTGCCACCA GATTCCCTT AGCTTCCACT	120
GTCTCCATGA GCTTTAAAAT GTGGGCGGCC GCTCGAGGGC TAGAGCGGCC GC	172

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 212 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (vii) IMMEDIATE SOURCE:

- (B) CLONE: SAC_24296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GGGGGATCCG CCCACTTGGC TGACCGCCAG GCGAGTGACT GTGACTCCAG GTTCGCCAC	60
TACCGCAGCA GATACTGCCT CGCCTATGCC ACCTTCATAG TAGTGGTCCT CCACGGTGAG	120
GATCCTGCCT TTGGTTGCTC TGGCACAGTC GAGAATGAGC TTTTTGTCCA GGGGCTTGAT	180
GGTGAAGGGG TCCAGTGGGC TAGAGCGGCC GC	212

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (vii) IMMEDIATE SOURCE:

- (B) CLONE: SAC_24445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GGGGGATCCG CCCACAGCAT TCGGGTATGA GGCAAGGGGA GTGTTCATTC ACACACACAG	60
TAGCTTCGGG TCTGTGAGGT CTCCTTGTTC CGGGTAGGT TTCTAAAGAC GGAGAAAAAA	120

ATGATTCTGG TTATCAAGAC TACTGTGACC GTATTAGATC CCAGAATGGG CAAGCATCAG	180
TGTGTGACCA TGCGAACAAA AGGAATTTTT	210

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: SAC_24527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGGGGATCCG CCCACCATGG TCTCACTCAG AGACGGGTTT GGTCAGTTTT AAGATGAACT	60
CCTTCGGATG TAGTGTCCGT AAGTCCTTAT TATCGCTGTC CATCAATTCA CGATAGGATA	120
GCTGGCTGCG GTGGCAAGTC CGCAGTGGTT GTTCCACCTG CCCACATTAT TCTCTCGTGG	180
CCATGGTTCT TCCCTTAGAG	200

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: SAC_24540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GGGGGATCCG CCCACAGTGG GAAGGATGGA AATAGCTGTC ATCTCTCAA AACTGAGTTC	60
CTTTCCTTCA TGAACACGGA GCTGGCCGCC TTCACGAAGA ACCAGAAGGA CCCCAGTGTC	120
CTCGACCGCA TGATGAAGAA GCTGGACCTC AACAGTGATG GGCAGCTAGA TTTCCAAGAG	180
TTTCTCAACC TTATTGGTGG CTTAGCTATA GCACCTGCC ACTCTCGTGG CTGGCCCTCT	240
GCTTATACTC CTTGGACTGC TCCAGGCTGT GTGTTCCAC GCTTGACCTG CCCACAGAGC	300
CAAAAGAGAC ACATTGGCTA CTTAAACCAC CTTAAAGCGG ACTCCAGGAA TATCACCCAC	360

GGCATGGCCT TTTGCGAAC AATCCCANCA ACCAAAAAAA

400

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: SAC_24623

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GGGGGATCCG CCCACAGTGC ATATTGGCGG CGCTCGCCTC ATTACGATTTC	60
TTCTCTTGTT CAATTGTTTC TTTTGAAGGC AGAGGGATTT TCTCTTGTGT	120
TTCAACTTCG ACTTATCGAA TTTCACCTGC CCACTAAACC CACAGCCCAG	180
TTCCCTCCTGT CCTGGAATTG	200

What is claimed is:

1. Purified and isolated nucleic acid encoding all or a unique fragment of a KIM.
2. Nucleic acid of claim 1 that is RNA.
3. Nucleic acid of claim 1 that is DNA.
4. Nucleic acid of claim 3 that is cDNA.
5. Nucleic acid that is complementary to the nucleic acid of claim 1.
6. Nucleic acid that hybridizes to the nucleic acid of claim 1 or 5.
7. Nucleic acid of claim 1 that is in operative association with an expression control element therefor.
8. Antisense nucleic acid of claim 1 that is sufficient, when internalized within a cell, to disrupt expression of a cellular KIM gene.
9. Purified and isolated nucleic acid encoding all or a unique fragment of a KIM, said nucleic acid having a sequence selected from the sequences listed in TABLE 1.
10. Purified and isolated nucleic acid encoding all or a unique fragment of a KIM, said nucleic acid having a sequence selected from degenerate variants of the sequences listed in TABLE 1.
11. Purified and isolated nucleic acid encoding all or a unique fragment of a KIM, said nucleic acid having a sequence selected from homologous variants of the sequences listed in TABLE 1.
12. Purified and isolated nucleic acid encoding a KIM fusion polypeptide, the sequence of said nucleic acid comprising a KIM sequence selected from the sequences listed in TABLE 1 fused in frame to a sequence encoding a non- KIM polypeptide.
13. Nucleic acid of claim 12 wherein the encoded non-KIM polypeptide is selected from: a secretable leader polypeptide, an immunoglobulin polypeptide, a binding pair partner, a toxin or toxoid, an enzyme, and a detectable polypeptide.

14. A vector comprising a KIM-encoding nucleic acid of any one of claims 1 to 13.
15. A host cell stably transformed or transfected with a vector of claim 14.
16. A method for producing a KIM polypeptide, comprising the steps of growing a host cell of claim 15 under conditions sufficient for the production of polypeptides of vector origin; and, recovering an expressed KIM polypeptide.
5
17. A purified and isolated polypeptide comprising all or a unique fragment of a KIM, said polypeptide having a sequence selected from the sequences encoded by nucleic acids listed in TABLE 1.
18. A purified and isolated polypeptide comprising all or a unique fragment of a KIM,
10 said polypeptide having a sequence selected from variants of the sequences encoded by nucleic acids listed in TABLE 1.
19. A polypeptide of claim 18 wherein said variant is a splice variant, truncation variant, or substitution variant of an encoded TABLE 1 sequence.
20. A KIM fusion polypeptide, the sequence of said polypeptide comprising all or a
15 unique fragment of an encoded KIM sequence listed in TABLE 1, fused to a non-KIM polypeptide sequence.
21. A fusion polypeptide of claim 20 wherein the non-KIM polypeptide sequence is selected from: a secretable leader polypeptide sequence, an immunoglobulin polypeptide sequence, a binding pair partner sequence, a toxin or toxoid sequence,
20 an enzyme sequence, and a detectable polypeptide sequence.
22. A conjugate comprising a KIM polypeptide of claim 17, 18 or 19, linked to a detectable moiety, imageable moiety, radiolabeled moiety, or toxin moiety.
23. A KIM fusion polypeptide, the sequence of said polypeptide comprising all or a unique fragment of an encoded KIM sequence selected from nucleic acid sequences
25 listed in TABLE 2, fused to a non-KIM polypeptide sequence.
24. A fusion polypeptide of claim 23 wherein the non-KIM polypeptide sequence is selected from: a secretable leader polypeptide sequence, an immunoglobulin

- polypeptide sequence, a binding pair partner sequence, a toxin or toxoid sequence, an enzyme sequence, and a detectable polypeptide sequence.
25. A conjugate comprising a KIM polypeptide of claim 23 or 24, linked to a detectable moiety, imageable moiety, radiolabeled moiety, or toxin moiety.
- 5 26. An antibody that binds selectively to all or a unique fragment of a KIM polypeptide encoded by a nucleic acid sequence listed in TABLE 1.
27. A conjugate comprising an antibody of claim 26, linked to a detectable moiety, imageable moiety, radiolabeled moiety, or toxin moiety.
- 10 28. An antibody that binds selectively to all or a unique fragment of a KIM polypeptide encoded by a nucleic acid sequence listed in TABLE 2.
29. A conjugate comprising an antibody of claim 29, linked to a detectable moiety, imageable moiety, radiolabeled moiety, or toxin moiety.
30. Use in therapy of an antisense KIM nucleic acid of claim 8.
31. Use in therapy of a KIM vector of claim 14.
- 15 32. Use in therapy of a KIM polypeptide of claim 17, 18 or 19.
33. Use in therapy of a KIM fusion protein of claim 20 or 21, or of a KIM conjugate of claim 22.
34. Use in therapy of an antibody of claim 26, or of an antibody conjugate of claim 27.
35. A pharmaceutical composition comprising a physiologically acceptable carrier having dispersed therein, to a therapeutically effective concentration: a KIM nucleic 20 acid of claim 8; a KIM vector of claim 14; a KIM polypeptide of claim 17, 18 or 19; a KIM fusion protein of claim 20 or 21; a KIM conjugate of claim 22; an anti-KIM antibody of claim 26; or, an anti-KIM antibody conjugate of claim 27.
36. A method for detecting the presence or status of renal injury or of renal disease, comprising the step of measuring the concentration of a KIM polypeptide in a 25

- sample selected from serum, urine or urine sediment of an individual afflicted with, or at risk of developing, renal injury or an impairment of renal function.
37. A method for detecting the presence or status of an abnormal response to tissue injury or other stimulus, comprising the step of measuring the concentration of a KIM polypeptide in a sample selected from serum, urine or urine sediment of an individual afflicted with, or at risk of developing, an autoimmune response or abnormal tissue growth arising from or affecting renal tissue.
- 10 38. A method according to claim 36 or 37, wherein said measuring step involves contacting said sample with an anti-KIM antibody of claim 26 or 28, or with a conjugate of claim 27 or 29.
- 15 39. A kit for practice of the method of claim 36 or 37, comprising at least one reagent selected from: the anti-KIM antibody of claim 26; the anti-KIM antibody of claim 28; the conjugate of claim 27; and, the conjugate of claim 29.
40. A method for detecting the presence or status of renal injury or of renal disease, comprising the step of measuring the level of a KIM nucleic acid in a sample selected from serum, urine or urine sediment of an individual afflicted with, or at risk of developing, renal injury or an impairment of renal function.
- 15 41. A method for detecting the presence or status of an abnormal response to tissue injury or other stimulus, comprising the step of measuring the level of a KIM nucleic acid in a sample selected from serum, urine or urine sediment of an individual afflicted with, or at risk of developing, an autoimmune response or abnormal tissue growth arising from or affecting renal tissue.
- 20 42. A method according to claim 40 or 41, wherein said measuring step involves contacting said sample with a KIM nucleic acid of claim 9, 10 or 11; or with a nucleic acid probe that hybridizes to KIM nucleic acid of claim 9, 10 or 11; or with a nucleic acid having a sequence selected from sequences listed in TABLE 2; or with a nucleic acid probe that hybridizes to a nucleic acid listed in TABLE 2.

43. A kit for practice of the method of claim 40 or 41, comprising at least one reagent selected from: the KIM nucleic acid of claim 9, 10 or 11; or a nucleic acid probe that hybridizes to KIM nucleic acid of claim 9, 10 or 11; or a nucleic acid having a sequence selected from sequences listed in TABLE 2; or a nucleic acid probe that hybridizes to a nucleic acid listed in TABLE 2.
44. A method of imaging cells or tissue expressing or producing a KIM, comprising the steps of contacting the cells or tissue with an imageable KIM-binding reagent; and, imaging an accumulation of the KIM-binding reagent.
45. A method according to claim 44 wherein the cells or tissue are disposed in body tissue of an individual suspected of harboring an imageable locus of KIM expression and/or production.
46. A method of locating a tissue mass abnormally producing or expressing a KIM in an individual suspected of affliction with an abnormal tissue response to injury or other stimulus, comprising the step of: administering an imageable KIM-binding reagent to the individual; and, imaging said tissue mass within the body of the individual.
47. A method according to claim 44 wherein the tissue mass is a tumor arising from or affecting renal tissue of the individual.
48. A method of treating an individual afflicted with, or at risk of developing, a disease or condition contributed to or associated with a dysfunction or dysregulation of a KIM gene or protein, comprising the step of administering to the individual a pharmaceutical composition of claim 35.
49. A method of treating an individual afflicted with, or at risk of developing, a disease or condition beneficially affected by therapeutic administration of a KIM composition of the present invention, comprising the step of administering to the individual a pharmaceutical composition of claim 35.

50. A method according to claim 48 or 49 wherein the disease is a renal disease; or, the condition is an impairment of renal function.
51. A method of inhibiting the growth of KIM-expressing tumor cells, comprising the step of contacting the tumor cells with a pharmaceutical composition comprising involving the step of contacting the cells with: an antisense KIM nucleic acid of claim 8; a KIM fusion protein of claim 20, 21, 23 or 24; a KIM conjugate of claim 22 or 25; an antibody of claim 26 or 28; or an antibody conjugate of claim 27 or 29.
52. A method according to claim 36, 37, 40, 41, 45, 46, 47, 48, 49, or 50 wherein the individual is a human.

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 98/10547

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12	C12N15/62	C12N5/10	C12N1/21	C07K14/47
C07K16/18	C12O1/68	A61K31/70	A61K38/17	A61K39/395
A61K48/00	G01N33/577			

According to International Patent Classification(IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K C12Q A61K G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	N.H. LEE ET AL.: "Comparative expressed-sequence-tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth factor treatment" EMBL SEQUENCE DATABASE, 1 October 1995, XP002080245 Heidelberg, FRG EST109574 Rat PC-12 cells, NGF-treated (9 days) Rattus sp. cDNA clone PRNAT01 3' end, Accession no. H33500; -/-	5,6

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

° Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the International filing date but later than the priority date claimed

- "T" later document published after the International filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "&" document member of the same patent family

Date of the actual completion of the International search

12 October 1998

Date of mailing of the International search report

22/10/1998

Name and mailing address of the ISA

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Hornig, H

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	N.H. LEE ET AL.: "Comparative expressed-sequence-tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth factor treatment" EMBL SEQUENCE DATABASE, 1 October 1995, XP002080246 Heidelberg, FRG EST111059 Rat PC-12 cells, NGF-treated (9 days) Rattus sp. cDNA clone PRNBQ59 5' end; Accession no. H34282; ---	6
X	N.H. LEE ET AL.: "Comparative expressed-sequence-tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth factor treatment" EMBL SEQUENCE DATABASE, 1 October 1995, XP002080247 Heidelberg, FRG EST1111810 Rat PC-12 cells, NGF-treated (9 days) Rattus sp. cDNA clone RPNCM27 5' end, Accession no. H34674; ---	6
A	US 5 552 313 A (CALVET JAMES P ET AL) 3 September 1996 see the whole document	1-52
A	WO 95 26732 A (AMUR RESEARCH CORP ;CHASLOW FRED I (US)) 12 October 1995 see the whole document	1-52
A	BONALDO FATIMA DE M ET AL: "NORMALIZATION AND SUBTRACTION: TWO APPROACHES TO FACILITATE GENE DISCOVERY" GENOME RESEARCH, vol. 6, no. 9, September 1996, pages 791-806, XP002039972 see the whole document	1-52
P,X	WO 97 44460 A (BIOGEN INC ;SANICOLA NADEL MICHELE (US); BONVENTRE JOSEPH V (US)); 27 November 1997 cited in the application see the whole document	1-8, 35-52
P,X	M. TAKADA ET AL.: "The cytokine-adhesion molecule cascade in ischemia/perfusion injury of the rat kidney. Inhibition by a soluble P-selectin ligand" J. CLIN. INVEST., vol. 99, no. 11, 1 June 1997, pages 2682-2690, XP002079925 ROCKEFELLER UNIVERSITY PRESS, NEW YORK, US see the whole document	1-8

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 98/10547

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	T. ICHIMURA ET AL.: "Kidney injury molecule-1 (KIM-1), a putative epithelial cell adhesion molecule containing a novel immunoglobulin domain, is up-regulated in renal cells after injury" J. BIOL. CHEM., vol. 273, no. 7, 13 February 1998, pages 4135-4142, XP002079926 AM. SOC. BIOCHEM. MOL.BIOL., INC., BALTIMORE, US cited in the application see the whole document -----	1-8

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 98/10547

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
Please see Further Information sheet enclosed.
2. Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- The additional search fees were accompanied by the applicant's protest.
- No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 98/10547

Patent document cited in search report	Publication date	Patent family member(s)		Publication date
US 5552313 A	03-09-1996	NONE		
WO 9526732 A	12-10-1995	AU 2206495 A		23-10-1995
WO 9744460 A	27-11-1997	AU 3567697 A		09-12-1997

